923, App 3137, Ap 3137, Ap 4004, Ap 7231, App 7231, Ap 6406, Ap 7411, Ap 113778, Ap 4879, Ap

Sequence

Sequence Seq

13223, A 4723, Ap 24, Appl 5053, Ap 105, Ap 105, Ap 11, Appl 11, Appl 14, Appl 15, Appl 16, Appl 17146, Appl

Sequence Sequence

10351, A 10528, A 17150, A

Sequence

6279, Ap 7148, Ap

17, Appl

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US-09-198-452A-923

US-09-540-236-2874

US-09-134-001C-3137

US-09-134-001C-3137

US-09-134-001C-3137

US-09-134-001C-3137

US-09-489-039A-13778

US-09-489-039A-13778

US-09-134-000C-4723

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US-09-134-000C-405

US-09-134-000C-405

US-09-134-000C-5021

US-09-134-001C-3551

US-09-134-001C-3551

US-09-134-001C-3551

US-09-134-001C-3055

US-09-136-1373

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US-09-137-001C-3055

US-09-134-001C-5055

US-09-134-001C-5055

US-09-134-001C-5055

US-09-134-001C-5055

US-09-138-33108

US-09-138-332-655

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US-09-252-991A-29547
US-09-489-039A-10777
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US-09-489-039A-13595
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US-08-900-230-2
US-09-058-333A-2
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US-09-154-874-9
US-08-931-668-9
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7407, Ap
8139, Ap
24727, A
346, App
2, App
17923, A
22003, A
22003, A
3341, Ap
3351, Ap
3350, App
2, Appli
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Sequence 8, Appli
Sequence 4, Appli
                                          September 16, 2004, 07:44:20 ; Search time 18 Seconds (without alignments) 108.988 Million cell updates/sec
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29293, A
27650, A
12581, A
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/cgn2 6/ptcdata/2/jaa/FOCMB.pep:*
/cgn2 6/ptcdata/2/jaa/PCTUS COMB.pep:*
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Compugen Ltd.
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US-09-364-230-8
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US-09-328-352-7407
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US-09-328-352-7407
US-09-328-352-7407
US-09-328-352-9134-5109
US-09-489-039A-9294
US-09-489-039A-9294
US-09-552-991A-17923
US-09-134-0011-3241
US-09-134-0011-3241
US-09-134-0011-3241
US-09-134-011-3241
US-09-134-011-3418
US-09-134-1361
                                                                                                                                        Total number of hits satisfying chosen parameters:
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  GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 100 summaries
                               - protein search, using sw model
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Perfect score:
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Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 17, Appl Sequence 3055, Ap Sequence 7202, Ap Sequence 7202, Appl Sequence 7202, Appl Sequence 13474, Appl Sequence 13474, Appl Sequence 13474, Appl Sequence 13474, Appl Sequence 11014, Appl Sequence 1014, Appl Sequence 1014, Appl Sequence 1014, Appl Sequence 10777, Appl Sequence 10777, Appli Sequence 2, Appli

Sequence 2, Appli Sequence 335, App Sequence 3409, Ap Sequence 9, Appli

Sequence 9, Sequence 9, Sequence 8,

Sequence 8

Sequence 8, Appl Sequence 7503, P Sequence 13595,

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Query Match
Best Local Similarity 52.9
Matches 18; Conservative
                                                                                                                                                                                                                                                                        21; Conservative
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
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US-09-328-352-8139
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US-09-328-352-7407
                                                                                                                            LENGTH: 360
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; Sequence 8, Application US/09364230
; Sequence 8.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rines, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
TILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT APPLICATION NUMBER: 05/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
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                                                                                      Sequence 72.7.4

Sequence 72.7.4

Sequence 72.7

APPLICANT Origene Technologies, Inc

APPLICANT Origene Technologies, Inc

APPLICANT ORIGENE TECHNOLOGIES, Inc

TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides

FILE REFERENCE: 1U 103 R.

CURRENT APPLICATION NUMBER: US/10/164,595

CURRENT FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.1

ENGTHA: 547
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Pred. No. 1.2e-09;
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09364230 Patent No. 6348339 GENERAL INFORMATION:
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ilarity 64.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 345
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Glycine max US-09-364-230-8
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US-09-364-230-8
                                                                                    US-10-164-595-72
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Matches
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Sequence 8139, Application US/09328352

Fatent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 8139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7407, Application US/09328352

Sequence 7407, Application US/09328352

Sequence 7407, Application US/09328352

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7407
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
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Best Local Similarity 52.8%; Pred. No. 1.5e-06;
Matches 19; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.0%; Score 106; DB 4; Length 299; 52.9%; Pred. No. 3.7e-07;
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63.6%; Pred. No. 1.3e-08;
tive 4; Mismatches 8
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                                 FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Acinetobacter baumannii
US-09-328-352-8139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-7407
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RESULT 8
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US-09-198-452A-376
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                              Sequence 5109, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A DOUCETTE-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILLING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILLING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
ATONNEY/AGENT INFORMATION:
NAME: ATIMICALION PAMELA:
NAME: ATIMICALION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
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LOCATION: (B) LOCATION 1...299;
SEQUENCE DESCRIPTION: SEQ ID NO: 5109:
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 5109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.9°
....hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
                                                                                                 US-09-107-532A-5109
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                                                                             RESULT 6
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REPERNCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GALVASON SOLUSION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEEC ACID AND PAINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REPERRACE: 2709,22004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PILING CATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                     Length 295;
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42.5%; Score 85; DB 4; Length 204
Best Local Similarity 42.1%; Pred. No. 0.00022;
Matches 16; Conservative 10; Mismatches 12; Indels
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42.0%; Score 84; DB 4; Length 304
Best Local Similarity 63.0%; Pred. No. 0.0005;
Matches 17; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                               49.0%; Score 98; DB 4; Le
52.9%; Pred. No. 4.9e-06;
Live 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; FRIOR APPLICATION NUMBER: US 60/074,788; FRIOR FILING DATE: 1998-02-18; FRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SOU ID NO 24727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9424, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 376, Application US/09198452A
Patent No. 6559294
                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24727
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Best Local Similarity 52.9°
Matches 18; Conservative
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; sequence 17923, Application US/09252991A; sequence 17923, Application US/09252991A; sequence 17923, Application US/09252991A; sequence 17923, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
; FILE REPRENCE: 1079-6.136; CURRENT FILING DATE: 1999-02-18; PRIOR PAPLICATION NUMBER: US 60/074,788; PRIOR PLING DATE: 1998-02-18; PRIOR PLING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 17923.
; SEQ ID NO 17923.
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Bacent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-ON NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22003. Application US/09252991A

Sequence 22003. Application US/09252991A

Sequence 22003. Application US/09252991A

Barent No. 6551795

GENERAL INFORMATION:

APPLICANT:

MATCH OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

REPERENCE:

107196.136

CURRENT APPLICATION NUMBER:

US 60/074,788

PRIOR APPLICATION NUMBER:

PRIOR PAPLICATION NUMBER:

PRIOR PAPLICATION NUMBER:

NOS 60/094,190

PRIOR PAPLICATION NUMBER:

SEQ 10 NO 22203

LENGTH: 221

LENGTH: 221
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37.5%; Score 75; DB 4; Length 221
Best Local Similarity 57.7%; Pred. No. 0.0065;
Matches 15; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
38.5%; Score 77; DB 4;
Best Local Similarity 47.1%; Pred. No. 0.0054;
Matches 16; Conservative 5; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FLGLGLMGSGIVSNLLKMGHTVTVWNRTABKCDL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 FAGLGLMGVPMCRRLLAAGYPLAVWNRSPGKREL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FLGLGLMGSGIVSNLLKMGHTVTVWN 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-252-991A-22003
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US-09-134-001C-3241
US-09-252-991A-17923
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Hitz, William D.

APPLICANT: Kinney, Anthony J.

APPLICANT: Kinney, Anthony J.

APPLICANT: Kinney, Anthony J.

APPLICANT: Rafalski, J. Antoni

TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids

TITLE OF INVENTION: Enzymes INVOlved in Degradation of Branched-Chain Amino Acids

CURRENT APPLICATION NUMBER: US/09/364,230

EARLIER APPLICATION NUMBER: 60/094,990

EARLIER APPLICATION NUMBER: 60/094,990

EARLIER FILING DATE: July 31, 1998

NUMBER OF SEQ ID NOS: 34
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40.2%; Score 80.5; DB 4; Length 307;
Best Local Similarity 31.0%; Pred. No. 0.0016;
Matches 18; Conservative 10; Mismatches 9; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch
1 Similarity 71.4%; Pred. No. 0.001;
15; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRT--
              LGLGLMGSGIVSNLLKMGHTVTVWNRT 29
                                                        IGLGAMGHAFASNLLKNGFTVAGWNRS 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 SNLLKMGHTVTVWNRTAEKCD 34
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                                                                                                                                                                                                      Sequence 2, Application US/09364230 Patent No. 6348339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE LOCATION: (247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE
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LENGTH: 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09584628
Patent No. 6309866
GENERAL INFORMATION:
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: 6-phosphogluconate dehydr
TITLE OF INVENTION: ogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/584,628
                                                                                                                                                                                                                                                                      GM10140
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,692
                                                                                                                                                                                                                                   36,795
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 474 amino acids
TYPE: amino acid
STRANDEDNESS: single
COPOLOGY: linear
US-09-058-692-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 474 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-09-584-628-2
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US-09-489-039A-8350

Sequence 8350, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
PAPPLICANT: GATY Breton et. al
TITLE OF INVENTION:
PILE REPERENCE: 2709-2004001

FILE REPERENCE: 2709-2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8350

IRRORT: 490

TYPE: PRI

CORGANISM: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
1 Similarity 38.2%; Pred. No. 0.023;
13; Conservative 10; Mismatches 11; Indels
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Patent No. 6162618
Patent No. 6162618
Patent No. 6162618

TITLE OF INVENTION: 6-phosphogluconate dehydr
TITLE OF INVENTION: 0genase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GVVGMAVMGRNLALNIESRGYTVSVFNRSREKTE 62
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FILING DATE: US/09/058,692
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3241
LENGTH: 474
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PA
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
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Matches 13; Conserv
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT FAPPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,990
BARLIER APPLICATION NUMBER: 60/094,990
BARLIER APPLICATION NUMBER: 60/094,990
BARLIER APPLICATION NUMBER: 05/094,990
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                                                                                                                                                                                                                                                                                                                                         Score 68; DB 4; Length 74;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                    APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NONBER: US/09/621,976
CURRENT FILING DATE: 2000.07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6407
LENGTH: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
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Pred. No.
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44 GFIGLGNMGSHMARNLVRAGYRVSV 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-364-230-12; Sequence 12, Application US/09364230; Patent No. 6348339; GENERAL INFORMATION:
                APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.0%; £
milarity 52.0%; E
Conservative 6;
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ilarity 37.1%;
Conservative
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Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: UNSURE
; LOCATION: (184)..(201)
US-09-364-230-12
                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-621-976-6407
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Matches 13; Conserv
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APPLICANT:
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                                                                                                                                                                                                                                                               TYPE: PRT
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Matches
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Sequence 26001, Application US/09252991A;
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS;
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS;
TITLE OF INVENTION: US/09/25,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26001
                                                                                                                                                                                                                            Sequence 5380, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
TITLE OF INVENTION: DIACNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIACNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
FRIOR PEDLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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36.5%; Score 73; DB 4; Length 474; 35.3%; Pred. No. 0.031; tive 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
36.0%; Score 72; DB 4; Length 486;
Best Local Similarity 34.4%; Pred. No. 0.044;
Matches 11; Conservative 12; Mismatches 9; Indels
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                                                                                                                   1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6407, Application US/09621976
Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Proteus mirabilis US-09-543-681A-5380
      36.5%
Query Match
Best Local Similarity 35.3%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 14; Conserv
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                                                                                                                                                                                                        RESULT 18
US-09-543-681A-5380
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LENGTH: 486
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Best Local
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Gaps

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Sequence 27650, Application US/09252991A

Patent No. 6521795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142'
SEQ ID NOS: 33142'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELATING TO KLEBSIELLA
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BPPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI

TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29
                                                                                                                                           DB 4; Length 154;
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                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 4;
Pred. No. 0.49;
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                                                                                                                                        Score 65;
Pred. No. 0
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                                                                                                                                                                                                                                                           2 FLGLGLMGSGIVSNLLKMGHTVTVWN 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12581, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 GTGLIGRHLIPRLLELGHSVTVSTR 38
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                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                      32.5%;
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                                                                                                             Query Match
Best Local Similarity 46.27
These 12; Conservative
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              RESULT 25
US-09-252-991A-27650
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                                                                                     US-09-252-991A-29293
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US-09-489-039A-12581
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LENGTH: 303
                   LENGTH: 154
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APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREI
THER REPERENCE: BLITTA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR PLING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 438
LENGTH: 292
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Patent No. 6521795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERABEUTICS
FILE OF INVENTION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR PRIOR DATE: 1998-02-18
PRIOR PRIOR DATE: 1998-02-18
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PRIOR PRIOR DATE: 1998-02-18
PRIOR DATE: 1998-02-18
PRIOR DATE: 1998-02-18
PRIOR DATE: 1998-02-18
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
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Pred. No. 0.12;
6; Mismatches 7; Indels
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0.21;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-364-230-6; Sequence 6, Application US/09364230; Patent No. 6348339
                                                                                                                                                                                                                                                                                                                                                            Query Match 33.5%;
Best Local Similarity 48.0%;
Matches 12; Conservative
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1 Similarity 52.0%;
13; Conservative
                                                                                                                                                                                                                                                             TYPE: PRT

CONGANISM: Escherichia coli

US-09-711-164-438
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; ORGANISM: Oryza sativa
US-09-364-230-6
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Matches 13; Conserv
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US-09-252-991A-29293
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APPLICATE INFORMATION:
APPLICATE: Lynn Doucette-Stamm et al
APPLICATE: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.5%; Score 61; DB 4; Length 352; 32.3%; Pred. No. 1.1;
                                                                        DB 4; Length 466;
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                                                                        Score 62; DB '
Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                          Sequence 3137, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3137
                                                                     Query Match 31.0%;
Best Local Similarity 42.3%;
Matches 11; Conservative
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Best Local Similarity 32.3%
Matches 10; Conservative
; ORGANISM: M.catarrhalis
US-09-540-236-2874
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US-09-134-001C-3137
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ORGANISM:
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Patent No. 6679910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILLING DATE: 2009-2005
CURRENT FILLING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3840
TYPE: PRT
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Redemote 923, Application US/09198452A

Redemote 923, Application US/09198452A

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999
                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-22004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10010
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0.53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.5%; Score 63;
Best Local Similarity 35.5%; Pred. No.
Matches 11; Conservative 7; Mismatcl
                                                      US-09-489-039A-10010
; Sequence 10010, Application US/094B9039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Klebsiella pneumoniae
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ORGANISM: Chlamydia pneumoniae
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Sequence 57891, A Sequence 11979, A Sequence 9081, Ap Sequence 5781, Ap Sequence 5781, Ap Sequence 12590, A Sequence 12590, A Sequence 13, Appli Sequence 1155, Ap Sequence 5105, Ap Sequence 12615, Ap Sequence 178316, Sequence 178316, Sequence 178316, Sequence 1688, Ap Sequence 255872, Sequence 1688, Ap Sequence 163370, App Sequence 163

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16, Appl
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116017,
14, Appl
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Sequence 16, Appl
Sequence 144794,
Sequence 144794,
Sequence 116017,
Sequence 14, Appl
Sequence 52389, A
Sequence 50561, A
Sequence 45255, A
Sequence 45255, A
                                                     2004, 07:45:18; Search time 48 Seconds (without alignments) 254.231 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                           1342398
                                                                                                 200
1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-067-482-3
US-10-067-482-3
US-10-067-482-4
US-10-167-5470-16
US-10-424-599-144794
US-10-437-963-116017
US-10-437-963-116017
US-10-167-5470-14
US-10-767-701-52389
US-10-282-122A-45255
US-10-282-122A-45255
                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                     1342398 segs, 321133274 residues
                                                                                       US-10-067-482-2_COPY_271_308
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Maximum Match 100%
Listing first 100 summaries
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                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2 US-10-369-493-11979
3 US-10-156-493-11979
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3 US-10-156-47190
3 US-09-815-242-5781
4 US-10-282-122A-47190
3 US-09-815-242-12581
5 US-10-282-122A-6339
5 US-10-282-122A-6339
6 US-10-282-122A-6339
7 US-09-738-526-5105
7 US-09-738-707-51011
7 US-09-728-122A-6715
7 US-10-282-122A-6715
7 US-10-369-493-1054
7 US-10-369-493-1054
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7 US-10-369-493-1056
7 US-10-424-599-2038
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12 15 15 12

Sequence 67753, A Sequence 11886, A Sequence 118134, Sequence 1951, A Sequence 1951, A Sequence 1961, A Sequence 2001, A Sequence 2002, A Sequence 2005, A Sequence 2005, A Sequence 200573, Sequence 200136, Sequence 200136, Sequence 200136, Sequence 200136, Sequence 2001374, Sequence 200142, A Sequence

53209,

Sequence Sequence

Sequence Sequence Sequence Sequence

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ORGANISM: homo sapiens
US-10-067-482-4
                                                                                                                                                           TYPE: PRT
' ORGANISM: Homo sapiens
US-10-103-313-417
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Sequence 72073, A Sequence 72092, A Sequence 72099, A Sequence 8044, Ap Sequence 43, Appl Sequence 77672, A Sequence 61885, A Sequence 61885, A Sequence 61885, A Sequence 61811, A Sequence 61811, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10067482; Publication No. US20030148407A1; GENBRAL INPORMATION: GENBRAL INPORMATION: APPLICANT: Oridene Technologies, Inc., TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene; FILE REFERENCE: 1U 102 R1; CURRENT FILIGHORATION NUMBER: US/10/067,482; CURRENT FILIGH DATE: 2002-02-07; NUMBER OF SEQ ID NOS: 4; SOFTWARE: Patentin version 3.1; SEQ ID NO 3; LENGIH: 547
                                                                                                                                                                                                                                            Sequence 2, Application US/10067482;
Publication Wo. US20030148407A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
FILE REFERENCE: 1U 102 R1
CURRENT APPLICATION NUMBER: US/10/067,482
CURRENT PILIG DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 553
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                                                   US-09-875-573-43

US-10-369-493-20932

US-10-282-122A-7672

US-10-282-122A-61885

US-10-767-01-41225

US-10-282-122A-61885

US-10-282-122A-70621

US-10-282-122A-70621
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    US-10-425-114-72073
US-10-425-114-72092
US-10-425-114-72099
US-10-369-493-8964
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100.0%; Pred. No. 1.5e-14;
trive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 32; Conservative
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Best Local Similarity 100.
Matches 38; Conservative
      4485
4485
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CORGANISM: homo sapiens
US-10-067-482-3
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: homo sapiens
     38.55
37.55
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US-10-067-482-2
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US-10-167-547C-16
US-10-167-547C-16
US-10-167-547C-16
Sequence 16, Application US/10167547C
Sequence 16, Application Wolfold Shall
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION NUMBER: US/10/167,547C
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 16
LENGTH: 289
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; Sequence 417, Application US/10103313;
publication No. US20030082758A1
GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
    FILE REFERENCE: PJZ07C1
    CURRENT FILING DATE: 2002-03-12
    NUMBER OF SEQ ID NOS: 653
    Prior Application removed - See File Wrapper or Palm
    SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 417
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82.0%; Score 164; DB 14; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 31; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.0%; Score 166; DB 14; Length 550; 100.0%; Pred. No. 1.5e-14; tive 0; Mismatches 0; Indels
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Sequence 4, Application US/10067482;
publication No. US20030148407A1;
GENERAL INFORMATION:
TITLE OF INVENTION: Applicaces behydrogenese Gene;
TITLE OF INVENTION: Anglogenesis Dehydrogenase Gene;
TITLE OF INVENTION: Anglogenesis Dehydrogenase Gene;
TITLE OF INVENTION: AUGUST.
CURRENT APPLICATION NUMBER: US/10/067,482;
CURRENT FILING DATE: 2002-02-07;
NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; SEQ ID NO 4
; LENGTH: 276
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Best Local Similarity 100.0
Matches 32; Conservative
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 116017
LENGTH: 343
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Sequence 14, Application US/10167547C

Sequence 14, Application US/101653A1

Sequence 14, Application US/101653A1

GENERAL INFORMATION:
APPLICANT: Brande, Howard G.
TITLE OF INVENTION: Butyrolacton and its intermediates

FILE REFRENCE: CLISQUE UNDERTION: Butyrolacton and its intermediates

TITLE OF INVENTION: Butyrolacton and its intermediates

CURRENT APPLICATION NUMBER: US/10/167,547C

CURRENT APPLICATION NUMBER: 60/297198

PRIOR APPLICATION NUMBER: 60/297198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.5%; Score 121, DB 16; Best Local Similarity 64.7%; Pred. No. 1.8e-08; Matches 22; Conservative 4; Mismatches 8;
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                                                                                 Sequence 116017, Application US/10437963 Publication No. US20040123343A1
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                                                                                                                      GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Too, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Ww. Wei
APPLICANT: Ww. Wei
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 55.34
Matches 21, Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 67
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US-10-167-547C-14
                                                              US-10-437-963-116017
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SEQ ID NO 14
LENGTH: 290
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APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: About String
APPLICANT: Cao Yunguei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DAIR: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Sequence 60840, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Caou, Yihua
APPLICANT: Caou, Yihua
APPLICANT: Caou, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERBNCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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                                           62.5%; Score 125; DB 14; Length 289; 60.5%; Pred. No. 4.1e-09; Live 4; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.0%; Score 124; DB 12; Length 333; Best Local Similarity 64.9%; Pred. No. 6.7e-09; Matches 24; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.5%; Score 121; DB 16; Length 176; 64.7%; Pred. No. 8.5e-09; ive 4; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_101768C.1.pep
US-10-424-599-144794
                                                                                                                                 1 GFLGLGLMGSGIVSNLLXMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                    4 GFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: 9298239.pep
US-10-767-701-60840
                                                                                                                                                                                                                                                                                        ; Sequence 144794, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                  Query Match
Best Local Similarity 60.5%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
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LENGTH: 333
US-10-167-547C-16
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Best Local S
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us-10-067-482-2_copy_271_308.rapb

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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 50561 LENGTH: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H.

PAPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITHA.034

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-110-23

PRIOR PILING DATE: 2000-110-23

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: LIB3136-019-H11_FLI.pep
US-10-425-114-50561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%; Score 117; DB 12;
63.6%; Pred. No. 7e-08;
iive 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52083, Application US/10282122A publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6'
Matches 21; Conservative
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Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-282-122A-52083
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LENGTH: 292
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APPLICANT:
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
FURE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NWERR: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72412C.1.pep
US-10-437-963-174476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), OTHER INFORMATION: Clone ID: 11922868.pep
US-10-767-701-52389
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Publication No. US20040034888A1
GENERAL INFORMATION
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                            La Rosa, Thomas J.

Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
Matches 21; Conserv
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US-10-425-114-50561
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US-10-767-701-52389
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LENGTH: 293
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APPLICANT:
APPLICANT:
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FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION: IMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/200,727
PRIOR PELICATION NUMBER: 60/200,727
PRIOR PELICATION NUMBER: 60/200,727
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/22,578
PRIOR PLICATION NUMBER: 60/25,625
PRIOR PELICATION NUMBER: 60/25,625
PRIOR PELICATION NUMBER: 60/25,636
PRIOR PELICATION NUMBER: 60/25,636
PRIOR PELICATION NUMBER: 60/25,636
PRIOR PELICATION NUMBER: 60/26,636
PRIOR PELING DATE: 2000-11-2-2
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-16
PRIOR PELI
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 290;
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Pred. No. 2.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Acinetobacter baumannii
                            Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.5%;
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Forsyth, R.
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                  Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                            Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.4
Local Similarity 59.4
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-282-122A-44990
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                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICANT:
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0
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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SOFTWARE: PatentIn version 3.1
                                                                               0;
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      54.5%; Score 109; DB 12; Length 292; 62.5%; Pred. No. 7.3e-07; 1ve 6; Mismatches 6; Indels
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53.0%; Score 106; DB 12; Length 288;
Best Local Similarity 55.6%; Pred. No. 1.9e-06;
Matches 20; Conservative 5; Mismatches 11; Indels
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                                                                                                                         1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                            9 GFIGTGVMGKGMIKULLKGGYTVHVYNRTKEK 40
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                     Sequence 45255, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR APPLICATION NUMBER: 60/200,347
PRIOR PLING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-01-02
PRIOR PLING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-112-27
PRIOR PLING DATE: 2000-112-27
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-09
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind, Judith
Wall, Daniel
                                                                      Conservative
Query Match
Best Local Similarity
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-10-282-122A-45255
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT ELITRA.034A
CURRENT FILIANG DATE: 2003-02-20
RIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATORI, WASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-06-30
SPRIOR APPLICATION NUMBER: JP 2001-272697
SPRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 56894, Application US/10282122A Publication No. US20040029129A1
                                         Sequence 9081, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9081
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                  APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.03
Matches 16; Conservative
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APPLICANT:
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Sequence 11979, Application WS/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Garagoury J.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Glater, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT RILING DATE: 2003-02-28

CURRENT FILING DATE: 2003-02-28
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          CURKENT APPLICATION NUMBER: US/10/282,122A
CURKENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-04
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-06
PRIOR PRIOR PLING DATE: 2001-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
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CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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; ORGANISM: Enterococcus faecium
US-10-282-122A-57891
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Best Local Similarity 52.9
Matches 18; Conservative
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LENGTH: 475
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LENGTH: 295
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42.1%; Pred. No. 0.0011; tive 9; Mismatches 13; Indels

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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                         16; Conservative
                                    Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                 US-09-815-242-5781
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FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PLICATION NUMBER: 60/191,078

PRIOR PELICATION NUMBER: 60/206,848

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-06

PRIOR PELING DATE: 2000-05-06

PRIOR PELING DATE: 2000-01-23

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 56894
LENGTH: 2.96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Enterococcus faecalis
US-10-282-122A-56894
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ORGANISM: Borrelia burgdorferi
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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44.0%; Score 88; DB 12; Length 464;

Query Match

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APPLICANT: Syskind, Judith W.
APPLICANT: Yaskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/201
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-34
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-22
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
4 GIYGLGVMGSNLALNIADNGFNVSVYNRDNEKTEIFVK 41
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44.0%; Score 88; DB 9;
Best Local Similarity 39.5%; Pred. No. 0.0011;
Matches 15; Conservative 12; Mismatches 11
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                        Sequence 5781, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant TAPPLICANT: Yamen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5781
                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
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APPLICANT: Cao Yongwei TTTLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION: 18-21 (53-223) B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 258895
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-22-3

PRIOR PILING DATE: 2001-22-6

PRIOR PILING DATE: 2010-20-09

PRIOR PILING DATE: 2010-20-09

PRIOR PILING DATE: 2010-20-09

PRIOR PILING DATE: 2011-27

PRIOR PILING DATE: 2011-21

PRIOR PILING DATE: 2011-22

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_75806C.1.pep
US-10-424-599-258895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43907, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 40.58
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Glycine max
Zhou Yihua
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
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44.0%; Score 88; DB 15
Best Local Similarity 36.8%; Pred. No. 0.0011
Matches 14; Conservative 13; Mismatches
                                                                                                             FRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SEQ ID NO 12590
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CURRENT FILING DATE: 2003-02-28
PRICA APPLICATION NUMBER: US 60/360,039
PRICH FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                 CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2943, Application US/10369493; Publication No. US20030233675A1
                                                            CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.55
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-10-369-493-2943
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LENGTH: 469
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US-10-282-122A-43907

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### APPLICANITY AU, H.

| TILE OF INVENTION: Identification of Essential Genes in Microorganisms
| FILE REFERENCE: ELITTA.034A
| CURRENT APPLICATION NUMBER: U5/10/282,122A
| CURRENT FILING DATE: 2000-03-220
| PRIOR APPLICATION NUMBER: 60/191,078
| PRIOR PILING DATE: 2000-03-21
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 2000-05-24
| PRIOR FILING DATE: 2000-05-26
| PRIOR PLICATION NUMBER: 60/207,727
| PRIOR FILING DATE: 2000-09-06
| PRIOR APPLICATION NUMBER: 60/230,335
| PRIOR PILING DATE: 2000-09-06
| PRIOR PILING DATE: 2000-09-09
| PRIOR PILING DATE: 2000-10-23
| PRIOR PILING DATE: 2000-11-27
| PRIOR FILING DATE: 2000-11-27
| PRIOR FILING DATE: 2000-11-27
| PRIOR FILING DATE: 2000-10-29
| PRIOR FILING DATE: 2000-10-29
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2001-02-09
| PRIOR FILING DATE: 2001-02-09
| PRIOR FILING DATE: 2001-02-09
| PRIOR PRILICATION NUMBER: 60/267,636
| PRIOR FILING DATE: 2001-02-09
| PRIOR PRILICATION NUMBER: 60/269,308
| PRIOR PILING DATE: 2001-02-09
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SOFTWARE: PatentIn version 3.1
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Pred. No. 0.0021;
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                                                                                                                                                                                                              Sequence 60359, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5105, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: AYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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Best Local Similarity 43.8%;
Matches 14; Conservative
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall, Daniel
Trawick, John
                                                                                                                                                                               US-10-282-122A-60359
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Publication No. US20040063181A1
GENERAL INFORMATION.
APPLICANT: Dunican, Rita
APPLICANT: Dunican, Rita
APPLICANT: Dunican, Rita
APPLICANT: Stapleton, Cliona
APPLICANT: Burke, Kevin
APPLICANT: Burke, Kevin
TITLE OF INVENTION: Process for the preparation of L-amino acids using
TITLE OF INVENTION: Process for the preparation of L-amino acids using
TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
CURRENT APPLICATION NUMBER: US/10/686,736
CURRENT FILING DATE: 2003-10-17
PRIOR FILING DATE: 2003-10-17
PRIOR FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 16
SOFTHARE: PatentIn Ver. 2.1
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APPLICANT: Stapleton, Cliona
APPLICANT: Burke, Revin
APPLICANT: Burke, Revin
APPLICANT: Burke, Revin
APPLICANT: Wockel, Bettina
TITLE OF INVENTION: Process for the preparation of L-amino acids using
FILE REFERENCE: 990229 BT-US-B
CURRENT APPLICATION NUMBER: US/10/078,167
NUMBER OF $\frac{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm{\pmathrm
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43.5%; Score 87; DB 12; Length 468;
Best Local Similarity 39.5%; Pred. No. 0.0015;
Matches 15; Conservative 12; Mismatches 11; Indels
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43.0%; Score 86; DB 12
Best Local Similarity 43.2%; Pred. No. 0.002;
Matches 16; Conservative 8; Mismatches
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US-10-686-736-3
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; ORGANISM: Corynebacterium glutamicum
US-10-078-167-3
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Publication No. US20030119154A1
GENERAL INFORMATION:
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Best Local Similarity 43.29
Matches 16, Conservative
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APPLICANT: McCormack, As
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US-10-686-736-3
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LENGTH: 459
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RESULT 30
US-10-767-701-61555
US-10-767-701-61555
Sequence 61555, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Enou. Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE REPERENCE: 38-21(53535)B
CURRENT FILLING DATE: 2004-01-29
CURRENT FILLING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 61555
LENGTH: 154
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42.5%; Score 85; DB 16; Length 154;
Best Local Similarity 40.5%; Pred. No. 0.00081;
Matches 15; Conservative 9; Mismatches 13; Indels
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                                                         APPLICANT: IKEDD, MASATO
APPLICANT: OZAKI, AKTO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE REPERRNCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/37484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VOY: 3.0
SEQ ID NO 5105
LENGTH: 492
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US-10-767-701-61555
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-5105
                       TATEISHI, NAOKO
SENOH, AKIHIRO
    YOKOI,
APPLICANT:
APPLICANT:
APPLICANT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 100 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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probable dehydroge D-threonin dehydro 3-hydroxyisobutyra

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2-hydroxy-3-oxopro probable 3-hydroxy 3-hydroxyisobutyra

probable glycerol-

probable 3-hydroxy probable 3-hydroxy probable sugar nuc probable sugar nuc

3-hydroxyisobutyra 3-hydroxyacid dehy hypothetical prote

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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laudinois, S.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Lee', S.M.; Lee', A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Y.; Roche, B.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon, Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sakiguchi, A.; Scavoska, A.; Error, T.; Winters, P.; Wiper, A.; Tanaka, T.; Terpstra, P.; Tagnoni, A.; Tosato, V.; Uchiyama, A; Authors: Poshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Tosato, V.; Uchiyama, A; Authors: Roshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Tosato, M.; Poshida, K.; Aitelerence number: A65880; MuID:98044033; PMID:9384377
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-288 ckun>A; Residues: 1-288 ckun>A; Residues: 1-288 ckun>A; Residues: Seperimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable dehydrogenase PA2199 [imported] - Pseudomonas aeruginosa (strain PAO1)
probables: Beeudomonas aeruginosa
C;Species: Beeudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Nov-2001
C;Accession: D8337, E. Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Ststover, C.K.; Pham, X.O.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82956, MUID:20437337; PMID:10984043
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A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: ykwC
C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
F,5-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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Best Local Similarity 52.9%; Pred. No. 1.3e-05;
Matches 18; Conservative 7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99; DB 2; 1
Pred. No. 9.6e-06;
8; Mismatches 12;
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Best Local Similarity 47.4%;
Matches 18; Conservative
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A; Status: preliminary
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3-hydroxyisobutyrate dehydrogenase homolog ykwC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: D5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: B69870
C;Accession: B69870
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter R;Kunst, F; Ogasawara, N; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chq A.; Bruilch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                        Cigeneties: Clostridium acetobutylicum Cigeneties: Clostridium Cigeneties: Clostridium Cigeneties: Clostridium Cigeneties: Clostridium Cigeneties: Clostridium Cigeneties: Clostridium acetobutylicum ATCC824

A; Residues: 1-292 kWIR>
A; Residues: 1-292 kWIR>
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A; Residues: Clostridium acetobutylicum ATCC824
C; Cenetics: Clostridium acetobutylicum ATCC824
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: G90314
C;Accession: G90314
R;K:, Confalonieri, F:; Zivanovic, Y:; Allard, G:; Awayez, M.J.; Char Jong, I:; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X:; Thi-Ngoc, H.P.; Redder, Jong, I:, Jeffries, A.C.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
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                                                                                                                                                                                                                       related to 3-hydroxyisobutyrate dehydrogenase, YKWC B. subtilis
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Pred. No. 4.3e-07;
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Local Similarity 58.8%; Pred. No. 5.8e-07;
Local Sobjective 7; Mismatches 7; Indels
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                                                   ALIGNMENTS
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1 Similarity 62.5%;
20; Conservative (
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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A;Gene: SSO1560
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dehydrogenase
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A;Cross-references: EMBL:X58719; NID:g47524; PIDN:CAA41555.1; PID:g47525
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
C;Keywords: oxidoreductase; pentose phosphate pathway
F;6-288/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: strain B31
C, Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate deh
                                                                                                                                                                                                                                                                                                                                                                                                                phosphogluconate dehydrogenase, decarboxylating (gnd) homolog - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 11-Jun-1999
C; Accession: H70169
C; Accession: H70169
C; Accession: Would be sequence_revision 13-Feb-1998 #text_change 11-Jun-1999
C; Accession: H70169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE001157; GB: AE000783; NID: 92688471; PIDN: AAC66918.1; PID: 9268847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: gnd
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate def
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cipecies: Staphylococcus aureus limporteul - Staphylococcus aureus (strain N315)
Cipecies: Staphylococcus aureus
Cipecies: Staphylococcus aureus
Cipecies: Staphylococcus aureus
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Circhia, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C.; Shiba, T.; Hatchori, M.; Osayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, 1. Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Accession: G89910
A; Status: preliminary
A; Mocession: G89910
A; Status: preliminary
A; Molecule type: DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                        Gaps
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                                                                                                                                       45.0%; Score 90; DB 1; Length 470; 43.2%; Pred. No. 0.00027; Live 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 468;
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                                                                                                                                                                                                                                                                         1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                        1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 44.0%; Score 88; DB 2;
Best Local Similarity 42.1%; Pred. No. 0.0005;
Matches 16; Conservative 9; Mismatches 13
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                                                                                                                                                                                          Conservative
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Best Local Similarity 39.5%
Matches 15; Conservative
                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Residues: 1-464 <KLE>
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R.Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe F. Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. A.Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                               A;Map position: 4
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;40-301/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome: plasmid
Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable D-threonine [imported] - Sinorhizobium meliloti (strain 1021) magar
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                               Gaps
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A)Residues: 1-334 <BEV>
A)Residues: 1-334 <BEV>
A)Cross-references: EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.150
A)Experimental source: cultivar Columbia; BAC clone F19B15
C)Genetics:
A)Gene: AFSP:F19B15.150
                                                                                                                                                                                                                                                         Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 293;
                                                                                                                                                                                                                                                 Score 92; DB 2; Length 334
Pred. No. 0.0001;
8; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB 2; I
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| ||||| : | || | : |||||| | | : || FLGTGLMGAPMARRLIGAGFSVTVWNRDAAKAE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
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Best Local Similarity 54.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Matches
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Oguch K.; F

RESULT 7 S1462B

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Riclaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; J. Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Scatus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: lin1413
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate del
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Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mahand, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
A,Accession. AH1246
A,Accession. AH1246
A,Molecule type: DNA
A,Molecule type: DNA
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C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphogluconate dehydrogenase homolog lmo1376 [imported] - Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: GB:AL592022; PIDN:CAC96644.1; PID:g16413886; GSPDB:GN00178
A, Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1246
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Pred. No. 0.00095;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 472;
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Pred. No. 0.00095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :|:|:|| : |: || GVIGMGVMGRNLALNIESRGHTVSIFNRSTEK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
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A;Cross-references: GB:NC_003210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 43.8%;
Matches 14; Conservative 9
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1 Similarity 43.8%;
14; Conservative
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Best Local S
Matches 14
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C; Species: Listeria innocua
C; Accession: ACISS8
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, L.; Dussurget, O.; Entian, K.D.; Fshhi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-885. U.
Science 294, 849-885. U.
R; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A; Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: ACISS8
A; Stelus: preliminary
A; Molecule type: DNA
A; Residues: 1-286 cGLA>
A; Cross-references: GB:AL592022; PIDN:CAC96235.1; PID:gl6413463; GSPDB:GN00178
A; Residues: 1-286 cGLA>
A; Generics:
C; Generics:
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A; Generics:
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A; Generics:
A; Generics:
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C; Generics:
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A; Generics:
C; Guperfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc
                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A/2200; MUD:99287316; PMID:10360571
A/Rocession: A/2777
A/Status: preliminary
A/Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Residues: 1-469 <ARN>
A.Gross-references: GB.AE001722, GB.AE000512; NID:g4980938; PIDN:AAD35523.1; PID:g498094
A.Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: TM0438
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
F;5-285/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6-phosphogluconate dehydrogenase homolog lin1413 [imported] - Listeria innocua (strain
                                                                                                                                                                     C. Species: Thermotoga maritima (Strain MSB8) (C. Species: Thermotoga maritima (strain MSB8) (C. Species: Thermotoga maritima (Strain MSB8) (C. Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 (C. Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 (C. Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 (C. D. Hickey R. Maleon, K. E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Darett, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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40.5%; Pred. No. 0.00055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.0%; Score 88; DB 2; L 36.8%; Pred. No. 0.00051; tive 13; Mismatches 11;
                       GVIGLAVMGKNLAWNIESRGYSVSVFNRSSEKTDLMVE
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Conservative 1
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 14; Conserv
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A; Molecule type: DNA

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C;Genetics:
A;Gene: TC0333
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
F;6-285/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
      A;Cross-references: GB:AE002301; GB:AE002160; NID:G7190372; PIDN:AAF39196.1; PID:G719037.
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Wolecule type: DNA
A,Residues: 1-29 <KOM>
B,Battnental Source: strain Kl2, W3110

R,Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A, Rose, D.J.; Mau, B.; Shao, Y.

A,File: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617; PMID:9278503
A,Accession: A65102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Escherichia coli (strain K-12
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
C;Keywords: oxidoreductase
F;8-269/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000394; GB:U00096; NID:g2367197; PIDN:AAC76159.1; PID:g1789513; A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000007; PIDN:BAB37426.1; PID:913363476; GSPDB:GN00154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli NyAlernate names: hypothetical 31K protein (rnpB-sohA intergenic region) C.Species: Escherichia coli C.Species: Escherichia coli C.Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002 R;Komine, Y: Inokuchi, H.

R;Komine, Y: Inokuchi, H.

Submitted to JIPID, September 1990
A;Reference number: JQ0612
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Pred. No. 0.00092;
                                                                                                                                                                                                                                   Length 479;
                                                                                                                                                                                                             Query Match
42.5%; Score 85; DB 2; Length 479
Best Local Similarity 39.5%; Pred. No. 0.0013;
Matches 15; Conservative 11; Mismatches 12; Indels
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Matches 19; Conserv
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C;Accession: C72088; H81581
Nature Genet. 21, 385-399; 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule Lype: DNA
A; Residues: 1-479 <ARN>
A; Residues: 1-479 <ARN>
A; Cross-references: GB:AE001620; GB:AE001363; NID:g4376631; PIDN:AAD18504.1; PID:g437663
A; Experimental source: strain CWL029
B; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, A; Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A; Fittle: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Residues: 1-479 <REA>
A:Cross-references: GB:AE002201; GB:AE002161; NID:g7189316; PIDN:AAF38243.1; PID:g718932
A:Experimental source: strain AR39, HL cells
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Avicle: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Residues: 1-479 <STO>
A;Cross-references: GB:BA000008; NID:gB978732; PIDN:BAA98568.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: gnd
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyxate
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                                                                                                                                                                                                                                   Length 479;
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Pred. No. 0.0013;
12; Indels
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1 Similarity 42.1%; Score 85; DB 2; Length 479;
1 Similarity 42.1%; Pred. No. 0.0013;
16; Conservative 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                                      42.5%;
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Best Local Similarity 42.13,
Then 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-479 <TET>
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C72088
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Rifinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Residues: 1-295 «KUR»
A;Residues: 1-295 «KUR»
A;Residues: 1-295 «KUR»
A;Residues: 1-295 «KUR»
A;Cross-references: GB:AL591985; PIDN:CAC49817.1; PID:g15141305; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC49817.1; PID:g15141305; GSPDB:GN00167
A;Experimental Bource: strain 1021, megaplasmid pSymB
A;Experimental Bource: strain 1021, megaplasmid pSymB
A;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
A;Authors: Kahn, M.L. Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizoblum meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho;
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Rychaeslan in 196736

Rytheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Chin, C.W.; Huter, J.L.; J. Huizar, L.

Nature 408

Rythrors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. P.; Southwick, A.M.; Sun, H.; Tallon, A; Atthes: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference number: A86141; MUID:21016719; PMID:11130712

A, Accession: D96736

A, Restructure and analysis of chromosome 1 of the plant Arabidopsis.

A, Rizzo, M.; Rowley, D.; Sakano, H. S.; Davis, R.W.

A, The: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A, Rizzo, M.; Rowley, D.; Rizzo, M.; M.; M.; Sun, H.; Tallon, A; Reference number: A86141; MUID:21016719; PMID:11130712
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A;Map position: 1
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                     probable dehydrogenase protein [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti (C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 299;
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46.9%; Pred. No. 0.0011;
iive 10; Mismatches 7
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Pred. No. 0.0011;
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Best Local Similarity 33.9%;
Matches 20; Conservative
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A;Genome: plasmid
C;Superfamily: 2-b
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A;Residues: 1-288 <AQF>
A;Cross-references: GB:AE000670; NID:g2982779; PIDN:AAC06408.1; PID:g2982783; GB:AE00065
A;Experimental source: strain VF5
C;Genetics:
A;Gene: hibD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable dehydrogenase yhaE [imported] - Escherichia coli (strain 0157:H7, substrain EDI probable dehydrogenase yhaE [imported] - Escherichia coli (5;Date: 16-Feb-2001 #text_change 14-Sep-2001 (5;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (5;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (5;Date: N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Tecession: C8533, 2001 enterchemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Cacession: C85374
A;Catesion: C85374
A;Catesion: Preliminary
A;Catesion: Preliminary
A;Catesion: C85374
A;Catesion: C853
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C;Species: Aquifex aeolicus
C;Daces: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Accession: C70303
R;Deckert, G.; Marren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
              A, Experimental source: strain 0157:H7, substrain RIMU 0509952
C, Genetics:
A, Gene: EC84003
C, Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:98196666; PMID:9537320
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strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                  Length
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Pred. No. 0.00092;
                                                                                                                                                                           Score 84.5; DB 2;
Pred. No. 0.00092;
9; Mismatches 9;
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Pred. No. 0.001;
5; Mismatches
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nilarity 32.8%;
Conservative 9
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32.8%;
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Best Local Similarity
Matches 16; Conserv
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Les 19; Conserv
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A; Status: prelimina
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                                                                                                                                                                                                                                                                    Matches
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C; Genetics:

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A;Gene: gntZ
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate deh
C;Keywords: oxidoreductase; pentose phosphate pathway
F;5-284/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) [imported] - Brucella melitensis (strain G;Species: Brucella melitensis (c;Species: Brucella melitensis (c;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 (c;Accession: AB3380 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkvov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesse Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensian A; Preference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AE008917; PIDN: AAL52205.1; PID: 917982987; GSPDB: GN00190
                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.0024;
5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GVIGLGVMGSNIALNMANKGENVAVYNYTRDLTDQLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                                                                                                                                             Score 83; DB 1;
                                                                                                                                                                                                                                                                                         41.5%;
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59.4%;
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32.8%;
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Matches 17; Conservative
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les 19; Conservative
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A;Molecule type: DNA
A;Residues: 1-291 <KUR>
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Best Local Similarity
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A; Residues: 1-294 < PAR>
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A; Residues: 1-468 cFUJ>
A; Rolecule type: DNA
A; Residues: 1-468 cFUJ>
A; Rolecule type: DNA
A; Residues: 1-468 cFUJ>
A; Rolecule type: DNA
A; Residues: 1-468 cFUJ>
A; Rolecules: GB: AB005554; GB: D45242; GB: D31629; NID: g2280496; PIDN: BAA21576.1; PI
R; Kunst, F: Broudillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
C.; Bron, S.; Broudillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S. D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A; Atthors: Founder, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Kathors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Msuda, S.; Maueel
Y; M.; Ogswa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                probable phosphogluconate dehydrogenase (gnd) - syphilis spirochete
C.Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C.Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C.Species: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 11-Jun-1999
C.Accession: A71337
R.Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.O.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A.Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A.Accession: A7137
A.Acces
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A;Experimental source: strain 168
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les 16; Conservative
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C;Superfamily: p
F;5-285/Domain:
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Matches
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2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) [imported] - Salmonella enterica subsp. C. Species: Salmonella enterica subsp. enterica serovar Typhi A.Note: this species has also been called Salmonella typhi G.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 R.Parkhill, J. Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Matuhors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; Accession AE0897
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
A,Map position: I
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                          Length 291;
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                                                                                                                                                      Score 82.5; DB 2;
Pred. No. 0.0017;
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Pred. No. 0.0017;
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Query Match
Best Local Similarity 41.73
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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A;Map position: 1
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
                                                                                                                                                                                                                                 hypothetical protein ywjF [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C; Species: Lactococcus lactis subsp. lactis C; Date: 23-Mar-2001 #text_change 03-Aug-2001 C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C; Accession: G86901 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sq A; Reference number: A86625; MUD:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005176; PID:g12725281; PIDN:AAK06313.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ywje:
C;Genetics:
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hq
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                                                             --AEKCDLFI 37
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21;
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Pred. No. 0.002;
8; Mismatches 11; Indels
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Indels
10;
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41.0%; Score 82; DB 2;
Best Local Similarity 43.8%; Pred. No. 0.002;
Matches 14; Conservative 11; Mismatches
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       Conservative
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A;Molecule type: DNA
A;Residues: 1-293 <STO>
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A; Residues: 1-297 <STO>
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   19;
       Matches
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RESULT 29

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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell: Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: C97687
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
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C,Superfamily: 3-hydroxyisobutyrate dehydrogenase, 3-hydroxyisobutyrate dehydrogenase hom
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C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumm
A, Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-threonine dehydrogenase (AB015439) [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                               ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule_type: DNA
A;Residues: 1-300 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88452.1; PID:g15157953; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-300 <KUR>
A;Cross-references: GB:ABG008688; PIDN:AAL43718.1; PID:g17741249; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
oxidoredutase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AH2912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 82; DB 2;
Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: September 16, 2004, 07:46:30 Job time : 16 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.0%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.0%;
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Q9chu6 lactococcus P96789 lactococcus P31337 homo sapien	083973 treponema p P29266 rattus norv 099113 mms mmsemlu	Q97id6 clostridium P52209 homo sapien Q9dcd0 mus musculu	ovis ar	F/1101 escherichia P/1775 escherichia	P45364 Clostridium P32185 oryctolagus	P52208 synechocyst	P41572 drosophila	P415/3 drosophila 09z751 chlamydia p	Q8r9j3 thermoanaer O67049 amiifex aeo	P41581 citrobacter P41582 citrobacter	P41574 escherichia P41575 klebsiella	P41577 klebsiella Q9zhd9 buchnera ap	O27957 archaeoglob O53814 mycobacteri	P41583 citrobacter	P41579 shigella dy P41580 shigella so	Q12680 saccharomyc	Q16636 NOMO Sapien Q61425 mus musculu	P00348 sus scrofa O9wwk7 rattus norw	Q821m8 chlamydophi	Q8pqu9 xanthomonas O89ax5 buchnera ap	Ogilcs bacillus an	P42205 pseudomonas P27412 rabbit hemo	P27413 rabbit hemo	P95113 mycobacteri	nterococ	acillus	Q8gcb0 bacillus me	099ul6 staphylococ	Q8nwm9 staphylococ	23939 Daciius su Q9kpq9 vibrio chol	Q89ww0 bradyrhizob	OSFILZ Chlamydia m OSF719 chlamydia t	Q883y4 pseudomonas	Q8pdy0 xanthomonas			neisseria	neisseri			
1 6PGD LACLA 1 6PGD LACLC 1 D3HI HUMAN			1 6PGD_SHEEP		D3HI	1 6PGD_SYNY3 1 DH3I_CAEEL	6PGD					1 6PGD_KLETE 1 6PGD_BUCAP			1 6PGD SHIDY 1 6PGD SHISO			1 HCDH_PIG 1 HCDH_RAT										GPDA		PANE				GPDA_XANCP ERG1_RAT				GALE		ALIGNMENTS	
472 472 336	335 335 335	332 482 482	482	297	32	482 299	481	334	330 269	445 445	445 445	445	269 294	445 445	445	2144	314	314	334	468	444	117	117	334	340 468	444	446 779	332	332	296	326	334	341	341 573	223	331	3 G 3 G 3 G 3 G	339			
36.5																																									
73 72 72	1 6 6 9 6 9 6	8 8 8 9 9 9 9 9	68	66.5	99	64 64	64	63	62 61	09	909	000	50 CO	5.59 5.99	93 93 1	58.5 58	580	58	0.0 0.0 0.0	9 G	57.5	57	57	57	57	56.5	56.5	26	5 5 5 5	55	5 1 2 1 2	22.0	55	25	54	54	54	54			
35.4		04 4 4 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	44	45	74	48	50	52	53	52	58	59	79	63	66	.9	69	71	72	74	75	77	B/ 62	0.8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	83	85	86		68	- 60	92	66	95	96	76	66	100			RESULT 1
gen Ltd.		(without alignments)	willow cell updates/sec		DLFIQ 38				141681						by chance to have a he result being printed, distribution				i bt	ч,	P21577 Synechococc O13287 candida alb	099ty2 staphylococ	Q931r3 staphylococ	O9pkx7 chlamydia m	P23523 escherichia	083351 treponema p	P52207 bacillus li	P32142 escherichia	P31072 trypanosoma	P43774 haemophilus	P80859 bacillus su	084066 chlamydia t	F38720 Saccharomyc P70718 actinobacil	P28811 pseudomonas	Obsuco arabidopsis	V8CP4/ stapnylococ O60037 cunninghame	754	576		702	P00350 escherichia P37756 shigella fl
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen	in search, using sw model	September 16, 2004, 07:31:17 ; Sear (without 197, 867, 867, 867, 867, 867, 867, 867, 86		US-10-067-482-2_COPY_271_308 200	GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ	162		41681 segs, 52070155 residues	ts satisfying chosen parameters:	ength: 0 ength: 200000000		Maximum Match 100% Listing first 100 summaries	BBProt 42.*		the number of results predicted by than or equal to the score of the ed by analysis of the total score d		SUMMARIES	5	nength DB AD	5 288	5 517 1 6PGD	0 468 5 324	5 468 1 6PGD	5 479 479	2 294 1 GARR	0 488 5 468	5 467 1 6PGD	0 298 1	0 479 1	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	5 468 1	4 4 80	5 484 1 6PGD	298 1	4 4 4 7	5 485 1 6PGD	468 1 6	468	9 481 1 6PGD_C	290 1 Y229	4 68
9	OM protein - protein	Run on: Sep		score: 20		Scoring table: BLC	,	Searched: 141	Total number of hits	Minimum DB seq leng Maximum DB seq leng	Parsaina.		Database : Swi		greatez		*	Result Oue		6 6 6	68	88	87	8 8 5	9 84.5	1 83	2 81	80	80	7 80	8 79	97 79	1 77	3 75	4 75	5 75	74	74	47.	31 73 36.5	3 73

976DD9098DB47A30 CRC64;

BY SIMILARITY

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Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
                      ACT SITE
SEQUENCE
                                                                                                                                                                                                                                      RESULT 2
6PGD_SYNP7
                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98044403; Pubmed-91843//;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

R. Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Barento V., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

R. Bourise K., Boursier L., Conletto N., Elyminels C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capiuano V., Carter N.M.,

R. Brouillet S., Bruschi C.V., Caldwell B., Capiuano V., Carter N.M.,

R. Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

R. Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

R. Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

R. Fritz C., Fujita M., Fabret C., Ferrari E., Foulger D.,

R. Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

R. Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

R. Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

R. Jozis B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

R. Kobayashi Y., Koctter P., Koningstein G., Krogh S., Kumano M.,

R. Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

R. Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

R. Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

R. Rieger M., Rivolta C., Schleich S., Schroeter R., Schione F.,

Schiguchi J., Scanlan E., Schleich S., Schroeter R., Schio B.,

Sorokin A., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A.,

R. Takeuchi M., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A.,

R. Yoshida K., Yoshikawa H., Vanamet K., Yasumoto K., Yata K.,

R. Yoshikawa H., Wandeler B., Wandeler H., Wanner E., Wasumoto K., Yata K.,

R. Yoshikawa H., Yamamoto H., Yamane K., Yasumoto K., Yasumone H., Yamane R., Yasumoto H., Hamane R., Yasumoto H., Hamane R., Yasumoto H., Hamane M., Harama H., Handeller M., Wannier P., Waller J., Wanneller M., Handeller M., Wanneller M., Wanneller M., Wanneller M., Wanneller M., Wanneller M., Wanneller 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.",
                                                                                                                                                                                                                                               STRAIN=168; Scanlan E.M.; Scanlan E.Devine K.M.; Scanlan E., Devine K.M.; Sequence of the Bacillus subtilis chromosome from ykuA to cse-15."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase ykwC (EC 1.1.-.-)
YKWC OR BSU13960.
                             288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; 6FGD.
InterPro; IPR006115; 6FGD.
InterPro; IPR006115; 6FGD NAD.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNĀSE.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ222587; CAA10859.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z99111, CAB13269.1, -. PIR, B69870, B69870. Subtilist; BG13328; ykwC.
                                 STANDARD;
                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=1423;
                             YKWC BACSU
034948;
                                                                                                                                                                                                                                                                                                                                                     STRAIN=168
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CONFLICT 154 158 EPIVR -> SRSVP (IN REF. 1).

CONFLICT 407 407 R -> A (IN REF. 1).

CONFLICT 415 440 AAERGIPVPAFSASLDFFDSYRASPA ->

RONFLICT 419 452 DYPG -> TTC (IN REF. 1).

CONFLICT 449 452 BYPG -> TTC (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Culler D.C., Krogmann D.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SUBSTRATE-BINDING SITE.
MEDLINE-90299831; PubMed=2113917;
Broedal S.E. Jr., Wolf R.E. Jr.,
"Genetic tagging, cloning, and DNA sequence of the Synechococcus sp.
strain PCC 7942 gene (gnd) encoding 6-phosphogluconate
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2). Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                     Length 288;
                                                     49.5%; Score 99; DB 1; Length 288
47.4%; Pred. No. 9.1e-06;
tive 8; Mismatches 12; Indels
                                                                                                                                                                             1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                   6 GFIGLGVMGKSMASHILNDGHPVLVYTRTKEKAESILQ 43
                                                                                                                                                                                                                                                                                                                                                                                                470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR006114; 6PGD_C.
Interpro; IPR006113; 6PGD_decarbox.
Interpro; IPR006115; 6PGD_ND.
Interpro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M55002; AAA27330.1; -.
EMBL; X59719; CAA41555.1; -.
EMBL; X1628; S14628.
HSSP; P00349; 2PGD.
InterPro; IPR008927; GDGH_C_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol, 172:4023-4031(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
288 AA; 30711 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGR00873; gnd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006183; 6PGD.
                                                                                                                           18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0873; gnd
PROSITE; PS00461; 6PGD;
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family.
                                                                                                                                                                                                                                                                                                                                                                                                   SYNP7
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aureus."
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=IFO 1060;
Watanabe M., Ishii N., Arisawa M., Aoki Y.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATEWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                           Length 470;
                                                   45.0%; Score 90; DB 1; Length 470 ilarity 43.2%; Pred. No. 0.00023; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.5%; Score 89; DB 1; Length 517; 39.5%; Pred. No. 0.00034; 1ve 9; Mismatches 14; Indels
   QW -> M (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91E3F520FFCABF7A CRC64;
                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                            517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006397; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
InterPro; IPR006118; 6PGD.
InterPro; IPR0061113; 6PGD_decarbox.
InterPro; IPR0061115; 6PGD_decarbox.
InterPro; IPR0061115; 6PGD_MAD.
InterPro; IPR006118; 6PGD_MAD.
InterPro; IPR006181; 6PGD_MAD.
InterPro; IPR006181; 6PGD_MAD.
InterPro; IPR006181; 6PGDPMAD.
Pfam; PF00393; 6PGD; 1.
Pfam; PF003946; MAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
                  470 AA; 50860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB006102; BAA21690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 AA; 56924 MW;
                                                                                                                                                                                                                                                                                                                                                                        Candida albicans (Yeast).
                                                                                                                                                                                                                                                   STANDARD;
   469
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                    16;
                                                                                                                                                                                                                                                 CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
CONFLICT
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                   Matches
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0
                                                                                                                                                                                               MEDLINE=21311952; PubMed=11418146;

KULOda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakwa H., Kubara S., Goto S., Yabuzaki J., Kanchisa M.,

Yamashita A., Oshima K., Furawa K., Yoshino C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lancet 359:1819-1827(2002)
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MW2;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Naqai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui b.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 AA; 51802 MW; 61A5C2CAF3CCD011 CRC64;
                                                                               Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.0%; Score 88; DB 1; 39.5%; Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006114; 6PGD C.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_NAD.
Pfam; PR00393; 6PGD; 1.
Pfam; PF03446; NAD_binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                         Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 39.5%,
"Lahes 15; Conservative 1
                                                                   GND OR SA1342 OR MW1464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR00873; gn
PROSITE; PS00461; 6PGD;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acquired MRSA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38

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468 AA.

STANDARD;

RESULT 4 6PGD STAAN ID 6PGD STAAN AC Q99TY2;

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Gaps

; 0

1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38

15; Conservative

Matches

2

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29
196
95
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26
                                        Name=Short;
                                                                                                                                                                                                                                                                                                                                                     6PGD STAAM
                                                         family
                                                                                                                                                                                                 NP BIND
ACT SITE
VARSPLIC
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                               6PGD_STAAM
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                         RESULT
Ωp
                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                     REVISIONS, AND ALTERNATIVE SPLICING.
MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                    DOWNE; C9VBM6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
(EC 1.1.1.31) (HIBADH).
                                                                                                                                                                                                                                                                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Bradopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
  GVIGLAVMGKNLAWNIESRGYSVSVFNRSSEKTDLMVE 43
                               324 AA.
                                PRT;
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     systematic review.":
                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            Lewis S.E.;
                                 DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECWEKKITHGGVYGNGQAAKLCINNMTAISMIGVSEAMNLA
VRQGLDANVF -> KCRQGRPRVHGQEDHPLRRLWHGPGRQ
AVQQHDAGHLDDRCFGGHESGGAPGSRCQCLRRDHQLLHRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAIVDASYDEMTADGVNKDTIFIDSSTISPDLVKSLQKKIS
AKGARFIDAPVSGGVPGAEQATLTFMVGGTEAEYNAVKAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLGLGDLQPCARSLPQCPSQQGLRRRFLLGSDHQGSGSGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGORFQLTHPAGISGAQGLPVAVR (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR.2004 (Rel. 43, Created)
15-MAR.2004 (Rel. 43, Last sequence update)
15-MAR.2004 (Rel. 43, Last sequence update)
15-MAR.2004 (Rel. 43, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
8taphylococcus aureus (strain MuSO / ATCC 700699).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                             IsoId=Q9V8M5-2; Sequence=VSP_001281, VSP_001282;
SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE 3-HYDROXYISOBUTYRATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1. Hypothetical protein; Oxidoreductase; NAD; Mitochondrion; Transit peptide; Alternative splicing.
TRANSIT 1 25 MITOCHONNBION (PV CHANSICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 324 Missing (In isoform Short).
/FTIG-VSP_001282.
324 AA; 33883 MW; A338534753EAE83E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAD (ADP PART) (POTENTIAL).
                                   methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87; DB 1; Le
Pred. No. 0.0004;
8; Mismatches 10;
                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP 001281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 GFVGLGNMGANMASNLIKAGHKLHVFDISKPACD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                           IsoId=Q9V8M5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBGN0034390; CG15093.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; GFGD.
InterPro; IPR006115; GFGD.
Pfam; PF03446; NAD binding_2; 1.
PRINTS; PR00076; GFGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003798; AAF57638.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003798; AAM68444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
324
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196
227
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MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nalsan W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; 'Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PKX7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.11.44)
GND OR TC0333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
43.5%; Score 87; DB 1; Length 468;
Best Local Similarity 39.5%; Pred. No. 0.00057;
Matches 15; Conservative 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 AA; 51783 MW; 07205599873133D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|| :|| : |: |: |: |: | : | : | GVIGLAVMGKNLAWNIESHGYSVSVFNRSSEKTDLMVE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006193; 6DGDH C like.
InterPro; IPR006193; 6FGD.—
InterPro; IPR006194; 6FGDGm BS.
InterPro; IPR006194; 6FGD C.
InterPro; IPR006113; 6FGD C.
InterPro; IPR006113; 6FGD decarbox.
InterPro; IPR006113; 6FGD NAD.
Ffam; PP00393; 6FGD, 1.
Ffam; PP03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNĀSE.
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PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                  Lancet 357:1225-1240(2001).
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           RAPARA RA
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CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                         -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6-phosphogluconate dehydrogenase, decarboxylating (BC 1.1.1.44).
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PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.5%; Score 85; DB 1; Length 479 39.5%; Pred. No. 0.0011; tive 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 AA; 52689 MW; 3501DD6DAA0B8F8B CRC64;
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                                                           -!- PATHWAY: Hexose monophosphate shunt.
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InterPro; IPR006115; 6PGD_ND.
InterPro; IPR006115; 6PGD_ND.
InterPro; IPR0061184; 6PGdom_BS.
Pfam; PF00393; 6PGD, 1.
Pfam; PF00393; 6PGD, 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
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InterPro; IPR006183; 6PGD.
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092613; 0940C1;
092613; 0940C1;
30-MAY-2000 (Rel. 39, 0
10-0CT-2003 (Rel. 42, 1
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TIGR; TC0333; -.
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SEQUENCE 479 AA
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6PGD_CHLPN
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B3125 OR C3880.
                           Escherichia coli, and Escherichia coli 06.
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                               Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate semialdehyde reductase) (TSAR).
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Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
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InterPro; IPR006113; 6PGD G.
InterPro; IPR006113; 6PGD NAD.
InterPro; IPR006118; 6PGD NAD.
InterPro; IPR006184; 6PGD NAD.
Pfam; PF00393; 6FGD; 1.
PRINTS; PR0346; NAD Pinding 2; 1.
PRINTS; PR00076; 6PGDHDK0NASE.
TIGRPAMS; TIGR00873; gnd; 1.
         Nucleic Acids Res. 28:1397-1406(2000).
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InterPro; IPR006183;
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Best Local Similarity
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SEQUENCE FROM N.A.
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01-NOV-1991
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GARR_ECOLI
ID _GARR_ECOLI
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                                                                                                                                                                                                                                                                                                   Komine Y., Inokuchi H.;
"Precise mapping of the rnpB gene encoding the RNA component of RNase
P in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=06.H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S., -R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Roso D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterization of the (D)-glucarate/galactarate catabolic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 182:2672-2674 (2000).
-!- CATALYTIC ACTIVITY: (R)-glycerate + NAD(P) (+) = 2-hydroxy-3-oxopropancate + NAD(P)H.
-!- PATHARY: D-galactarate metabolism; third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98447507; PubMed=9772162;
Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;
"Evolution of enzymatic activities in the enclase superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR002204, 3hydroxisobut_dh.
InterPro, IPR006183, 6PGD.
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EMBL; U18997; AAA57928.1; ALT INIT.
EMBL, AE000394; AAC76159.1; ALT INIT.
EMBL; AE016767; AAN62321.1; ALT INIT.
ECOGENE; EG11176; GARR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20225875; PubMed=10762278;
                                                                                                                                                                                                                                                                                                                                                                                            n Escherichia coli K-12.";
Bacteriol. 173:1813-1816(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in Escherichia coli.";
Biochemistry 37:14369-14375(1998)
                                                                                                                                                                                                                                                                               MEDLINE=91154140; PubMed=1705543;
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                                                                                                                                                                                              SEQUENCE FROM N.A.
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Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                          488 AA; 52767 MW; FB69CCCA98DEE6B5 CRC64;
                                            Complete proteome. SEQUENCE 488 AA;
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          S KW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                  21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNU OK 1rvssı.
Treponema pallidum.
Bactexia; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                              42.2%; Score 84.5; DB 1; Length 294; 32.8%; Pred. No. 0.00077; ive 9; Mismatches 9; Indels 21
                       Pfam; PP03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
TIGRETAMS; TIGR01505; tartro sem red; 1.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
Oxidoreductase; NAD; Complete proteome.
ACT SITE 170 BY SIMILARITY.
SEQUENCE 294 AA; 30427 MW; 17DA392C2253278C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRT-----
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InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_NAD.
InterPro; IPR006184; 6PGdOm_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
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InterPro; IPR006183; 6PGD.
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   InterPro; IPR006398; Tartro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                          Query Match 42.2
Best Local Similarity 32.8
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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HSSP; P00349; 2PGD.
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083351;
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PEam; PR00393; 6PGD; 1.
Pfam; PR03446; NAD binding 2; 1.
PRINTS; PR000076; 6FGDINGNASE.
TIGREPMS; TYCR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.

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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brisch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Maga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Maga K., Haiech J., Labunchard M., Klein C.,
RA Kobayashi Y., Kocheter P., Koningstein G., Kroph S., Kumano M.,
RA Kurita K., Lapidus A., Latdinois S., Lauber J., Lazarvic V.,
RA Kobayashi Y., Mellado R.P., Mixuno M., Moestl D., Nekai S., Noback M.,
RA Medina N., Mellado R.P., Mixuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Takeuchi M., Tamakoshi A., Taragi T., Takahashi H., Takemaru K.,
RA Sorokin M., Tamakoshi A., Tanakoshi A., Taragi T.,
RA Takai A., Wanbutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Wanbutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Wanbutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamamoto H., Yasamoto K., Yasamoto K., Yasamoto S., Vandenbol M., Voshikawa H.F., Zusumeten E., Poshikawa H.F., Zusumeten E., Poshikawa H.F., Zusumeten E., Poshikawa H.F., Danchin B., Schrotin R., Poshikawa H.F., Zusumeten E., Poshikawa H.F., Danchin R., Poshikawa H.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96093926; PubMed=7584049;
Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;
Cloning and sequencing of a 36-kb region of the Bacillus subtilis genome between the gnt and iol operons.";
DNA Res. 2:61-69(1995).
                                                                                                                                                                                                                                                                                        01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87008613; Pubmed-3020045; Pujita Y., Fujita T., Miwa Y., Nihashi J., Aratani Y.; "Organization and transcription of the gluconate operon, gnt,
                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                  1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                            6 GFIGLAVMGENLVLNIERNGFSVAVFNRTTTVVDRFL 42
         Score 84; DB 1;
Pred. No. 0.0015;
8; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 261:13744-13753(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
           42.0%;
Query Match
Best Local Similarity 43.2°
Matches 16; Conservative
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / BGSC1A1;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=1423;
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01-0CT-1989
01-0CT-1989
10-0CT-2003
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Similarity
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SEQUENCE FROM N.A.
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 STRAIN=BGSC5A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Simi
                                                                                                                  family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIHU_ECOLI
                                              operon.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P32142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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В
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                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                               MEDLINE=92065803; PubMed=1659648;
Reizer A., Deutscher J., Saier M.H. Jr., Reizer J.;
"Analysis of the gluconate (gnt) operon of Bacillus subtilis.";
Mol. Microbiol. 5:1081-1089(1991).
---- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (BC 1.1.1.44).
                                                                                                                                                                                    -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                        Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
"36kb sequence between gntZ and trnY of B. subtilis genome.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.5%; Score 83; DB 1; Length 468;
44.7%; Pred. No. 0.0019;
ive 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 AA; 51983 MW; 56D88BEB8E553856 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 AA
                                                                                                                                                                                                                                                                                                                                                                                             Subtilist, BG10651; gntZ.
InterPro; IPR00827; GD3H_C_like.
InterPro; IPR006183; GD3H_C_like.
InterPro; IPR006114; GPGD_C.
InterPro; IPR006114; GPGD_C.
InterPro; IPR006115; GPGD_GCarbox.
InterPro; IPR006115; GPGD_NAD.
InterPro; IPR006118; GPGdOM_BS.
Pfam; PF003446; NAD binding 2; I.
PRNNTS; PR00076; GFGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                                           EMBL, J02584; AAA56927.1; -.
EMBL, AB005554; BAA21576.1; -.
EMBL, 299124; CAB16045.1; -.
EMBL, D78193; BAA11267.1; -.
PIR, D26190; D26190.
                                    SEQUENCE OF 460-468 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGR00873; gnd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 44.7
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
   subtilis.";
Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEÇUENCE FROM N.A.
                                                                                                        PROBABLE FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
SEQUENCE 468 AA
                                                STRAIN=168;
                                                                                                                                                                                                             family.
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BACLI
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6PGD_BA
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                                                                                                                                  DAR Res. '1:157-162 (1994).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
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SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=93347969; PubMed=8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
"Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";
                                    Yoshida K., Seki S., Fujita Y.; "Nucleotide sequence and features of the Bacillus licheniformis gnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.flexmeri, STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                       -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.5%; Score 81; DB 1; Length 467
42.1%; Pred. No. 0.0035;
atrive 6; Mismatches 16; Indels
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01-OCT-1993 (Rel. 27, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT Apporterical oxidoreductase yihu (EC 1.1.-.-)
VIHU OR B3882 OR SF3954 OR S3792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 21:3391-3398(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006114; 6FGD_C.
InterPro; PR0066113; 6FGD_decarbox.
InterPro; IPR0066115; 6FGD_NAD.
InterPro; IPR006184; 6FGGGm_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P00349; 2PGD.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
WEDLINE=96051988; PubMed=8535972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D31631; BAA06504.1; -. PIR; JC2306; JC2306.
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PROSITE; PS00461; 6PGD; 1.
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Trypanosoma brucei
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NCBI_TaxID=5702;
                                                                                                                                                         family.
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P31072;
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"Utilization of dihydroorotate as sole pyrimidine source by Salmonella
                                                  "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                    SPECIES-S. Flexneri, STRAIN=2457T / ATCC 700930 / Serotype 2a; SPECIES-S. flexneri, STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=1.2704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., May B., Perna M.T., Payane S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Schwartz D.C., Blattner F.R.; Schwartz D.C., Statain 2457T.; Infect. Immun. 71:2775-2786 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Encogene, EG11847; yihu.

InterPro; IPR002204; 3hydroxisobut_dh.

InterPro; IPR00415; 6PGD NAD.

PRom; PF03446; NAD binding 2; 1.

PROSITE; PS00895; 3 HVDROXISOBUT_DH; 1.

Hypothetical protein, Oxidoreductase; NAD; Complete proteome.

ACT_SITE 171 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 80; DB 1; Length 298; 53.3%; Pred. No. 0.0031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
74FBC8C09FA7881C CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
18-EEB-2003 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase yihU (EC 1.1.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 AA
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EMBL, AAD000464; AAD13444.1; -.
EMBL, AEO15402; AAN45389.1; -.
EMBL, AEO16990; AAP18811.1; -.
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298 AA; 31158 MW;
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09L7S0;
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SEQUENCE
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Matches
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SEQUENCE FROM N.A.

STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MEDLINE=21534948; PubMed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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"A 6-phosphogluconate dehydrogenase gene from Trypanosoma brucei.";
Mol. Biochem. Parasitol. 57:89-100(1993).
                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
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MEDLINE=98411456; PubMed=9737929;
Phillips C., Dohnalek J., Gover S., Barrett M.P., Adams M.J.;
"A 2.8-A resolution structure of 6-phosphogluconate dehydrogenase.
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28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
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InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6FGD NAD.
InterPro; IPR006115; 6FGD NAD.
InterPro; IPR006015; NAD BS.
Pfam; PF03446; NAD binding_2; 1.
PR087ITE; P800895; 3 HYDROXYISOBUT_DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
ACT SITE 171 HY BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.0%; Score 80; DB 1; Length 298; 57.7%; Pred. No. 0.0031; ive 6: Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7ED9FA174249240C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 57.7%; Pred. No. 0.00
Matches 15; Conservative 6; Mismatches
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298 AA; 31280 MW;
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SEQUENCE
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6PGD_HAEIN
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                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            SUBUNIT: Homodimer. SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00461, 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                       EMBL; X65623; CAA46577.1; -. PIR; A48565; A48865. DDB; IDGJ; I1-NOV-99. InterPro; IPR008927; 6DGDH_C_like. InterPro; IPR006183; 6PGD. InterPro; IPR006113; 6PGD_C. InterPro; IPR006113; 6PGD_decarbox. InterPro; IPR0061113; 6PGD_decarbox. InterPro; IPR0061113; 6PGD_NAD. InterPro; IPR0061184; 6PGdom_BS.
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Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- РАТНИАŶ: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        52153 MW; 64FED260915ABC2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 80; DB 1; 39.5%; Pred. No. 0.0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] --
SEQUENCE FROM N.A. STCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; Pabmed=7542809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 39.5%
Matches 15; Conservative
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P43774;
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STRAIN=168;
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EMBL; Z73041; CAA97285.1; -.
PIR; S64588.
HSSP; P00349; 2PGD.
Germonline; 141568; -.
SGD; S0003488; GMD2.
GO; GO:0004616; Fiphosphogluconate dehydrogenase (decarboxyla. .; IMP. GO; GO:0006006; P:glucose metabolism; IGI.
InterFro; IFR008927; 6DGDH_C_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of a 10.5 kb DNA fragment from the yeast chromosome VII reveals the presence of three new open reading frames and of a tRNAThr gene.";
Yeast 13:369-372(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
88-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating 2 (EC 1.1.1.44).
GND2 OR YGR256W OR G9170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.

    PATHWAY: Hexose monophosphate shunt.
    SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase

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                                                                                                                                                                                                                                                      Pfam; PF0039; 6FGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR0076; 6FGDHDRONASE.
TIGREAMS; TIGRO0973; gnd; 1.
PROSITE; PS00461; 6FGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97279233; PubMed=9133741;
Mazzoni C., Ruzzi M., Rinaldi T., Solinas F., Montebove F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%; Score 80; DB 1; Length 484; 39.5%; Pred. No. 0.0049; tive 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 AA; 53140 MW; 8381EEB3C704C5DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                      InterPro; IPR008927; 6DGDH C_like.
InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR006116; 6PGD NAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
C64077; C64077.
                           HSSP; P00349; 2PGD.
TIGR; HI0553; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frontali L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6PG2_YEAST
ID _6PG2_YEAST
AC P533<u>1</u>9;
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A Kunst F., Ogsawara N., Absertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S., Borriss L., Brans A., Braun M., Brighell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Andriack S., Brischi C.V., Connerton I.F., Cummings N.J., Daniel R.A., Brian K.M., Dusterboft A., Ebrlich S.D., Emmerson P.T., Andriack K.D., Errick C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Anias S., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Hada K., Haicoth J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamatea D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamatea D., Kasahara Y., Klaerr-Blanchard M., Klein C., Andriack K., Lapidus A., Luu H., Masuda S., Mauel C., Medigue C., Media N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M., Roote B., M., Dertetelle D., Porwollik S., Prescott A.M., Raro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Reger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y., Sanlan B., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Schleich J., Tarkansh H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
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MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating II (EC 1.11.44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              3D75D53563987735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 GLVGLAVMGQNLILNAADHGFTVVAYNRTQSKVDRFL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.0%; Score 80; DB 1;
40.5%; Pred. No. 0.005;
Ative 6; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 AA
Interpro; IPR006183; 6PGD.
Interpro; IPR006114; 6PGD C.
Interpro; IPR006113; 6PGD decarbox.
Interpro; IPR006115; 6PGD NAD.
Interpro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                 Pfam; PP00393; 6PGD; 1.
Pfam; PP00346; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
IIGREAMS; TIGR00873; 9nd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbiology 142:3103-3111(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6PG2 BACSU STANDARD; P80859; P54546; 01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA; 53922 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 40.5
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
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Davis R.W.;
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P38720;
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6PG1_YEAST
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Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yasumoto K., Yashida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
                                                                                                                                                                                                                                                         "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                              Medigue C., Rose M., Viari A., Danchin A.; "Detecting and analyzing DNA sequencing errors: toward a higher quality of the Bacillus subtilis genome sequence."; Genome Res. 9:1116-1127(1999).
                                                                                                                                                                                                                                                                                                                           PATHWAY: Hexose monophosphate shunt.
SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
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0
                                                                                                                                                                                                                                                                                                                                                     family.
CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 41.
                                                                                                                                                                                                         STRAIN=168 / IS58;
MEDLINE=97443988; PubMed=9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00461; 6FGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.5%; Score 79; DB 1; Length 468; 36.8%; Pred. No. 0.0065; tive 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L -> W (IN REF. 4).
Q -> E (IN REF. 1).
; 75268F6ED400F1BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D84432; BAA12615.1; ALT_FRAME.
EMBL; 299116; CAB14318.2; -.
HSSP; P00349; 2PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mast, Forth 138; ygji.
Interpro; IPR006183; 6FGD.
Interpro; IPR006114; 6FGD.
Interpro; IPR006113; 6FGD.
Interpro; IPR006113; 6FGD.
Interpro; IPR006115; 6FGD.NAD.
Interpro; IPR006116; 6FGD.NAD.
                                                                                                                    MEDLINE=20036940; PubMed=10568751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468 AA; 51643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00873; gnd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                               Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                SEQUENCE OF 1-13
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61
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                                                                                                        REVISIONS
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Best Local {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INIT MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6PGD_CHLTR
ID 6PGD_CHL
AC 084066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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480 AA

PRT;

STANDARD;

CHLTR

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                                                                                                                                                                                                                                                                                                                 STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Attchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 282:754-759(1998).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
-!- PATHWAY: Heach CO(2) + NADPH.
-!- PATHWAY: Belongs to the 6-phosphogluconate dehydrogenase
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
6-phosphoglucomate dehydrogenase, decarboxylating 1 (EC 1.1.1.44).
GND1 OR YHR183W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
30-WAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GND OR CTOG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                 Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IRRO66114; 6PGD C.
InterPro; IRR066113; 6PGD—decarbox.
InterPro; IRR066113; 6PGD—decarbox.
InterPro; IRR066184; 6PGDm BS.
Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRONASE.
PRINTS; PR00076; 6FGDHDRONASE.
PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 AA; 52667 MW; E2D9BFE893DCECB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.5%; Score 79; DB 1; 36.8%; Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE001281; AAC67654.1; -.
PIR, A71561; A71561.
RSSP, P00349; 2PGD.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 36.8% hes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome
SEQUENCE 480 AA
                                                                                                                                                                                                                           NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ
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NCBI_TaxID=714;
                                                            6PGD ACTAC
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                                                                                 P70718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMSB PSEAE
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                                                            A PART A 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; $46671; $46671.

HSSP; $60349; 2PGD.

Germonline; 13930.

GO; $00004265; $GND1.

GO; $60:00045137; $C:cytoplasm; IDA.

GO; $60:0004616; $Fightosphogluconate dehydrogenase (decarboxyla. . .; IMP. GO; $60:000606; $P:dlucose metabolism; IGI.

InterPro; IPR008927; $60GDH_C_like.

InterPro; IPR006183; $6PGD_C_like.

InterPro; IPR006113; $6PGD_decarbox.

InterPro; IPR006115; $6PGD_decarbox.

InterPro; IPR006115; $6PGD_NAD.

InterPro; IPR006118; $6PGD_MAD.
                                                                                                                    STRAIN=5288C / AB972;
MEDLINE=94370803; Pubmed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
Latrellle P., Louis E.J., Macri C., Mardis E., Kenezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Mohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- CATAINTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-:- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                            "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=95003288; PubMed=7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.5%; Score 79; DB 1; Length 489; 40.5%; Pred. No. 0.0067;
                           Desouza M., Lobo Z., Maitra P.K.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55CAE5DACDC6A00B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 41-47 AND 120-131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z46631; CAA86600.1; -. EMBL; U00028; AAB68452.1; -. EMBL; U17155; AAAS3637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            Science 265:2077-2082(1994).
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SEQUENCE FROM N.A.
                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                        Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Matches
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-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97148607; PubMed=9020051;
Yoshida Y., Nakano Y., Yamashita Y., Koga T.;
"The gnd gene encoding a novel 6-phosphogluconate dehydrogenase and its adjacent region of Actinobacillus actinomycetemcomitans
                                                                                                                                                                                                                                                          6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH).
Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 AA; 53288 MW; F7BD0B2EA3BF624D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 GVIGLAVMGONLILNMNDHGFKVVAYNRTTSKVDEFLE 45
                                                                                                                                                                                                                                                                                                                                                                    Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                           Last sequence update)
Last annotation update)
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36.8%; Pred. No. 0.012;
ative 8; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JG5282; JG5282.
HSSP; P00349; ZPGD.
InterPro; IPR008927; GDGDH_C_like.
InterPro; IPR006183; GPGD.
InterPro; IPR006118; GPGD_C.
InterPro; IPR0061118; GPGD_C.
InterPro; IPR0061115; GPGD_C.
InterPro; IPR0061115; GPGD_NAD.
InterPro; IPR0061184; GPGD_NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03446; NAD binding 2; 1. PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D88189; BAA13558.1; -.
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STANDARD;
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Pfam; PF03446; NAD_bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosomal DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMSB PSEAE
P28811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC DIT DIT OF DI
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Gaps

· 0

16; Indels

6; Mismatches

1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37

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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAILE-20437337; PAO1;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Salar M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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09SUG0; QBLC25;
16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (EC 1.1.1.31) (HIBADH).
AT4G20930 OR T18K1.90
ATAG20931 thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                    Steele M.I., Lorenz D., Hatter K., Park A., Sokatch J.R.; Mcharacterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding methylmalonate-semialdehyde dehydrogenase and 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = methyl-3-oxopropanoate + NADH.
-!- PATHWAY: Distal valine metabolic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.5%; Score 75; DB 1; Length 298; llarity 57.7%; Pred. No. 0.014; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAD (BY SIMILARITY).
BY SIMILARITY.
0C4D7B5A7C870730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
PROSIDE; PS00895; 3 HYDROXYISOBUT DH; 1.
NAD Complete profeome NP BIND A NAD (BY SIMI
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                                                                                                                                                                                                                         hydroxyisobutyrate dehydrogenase.";
J. Biol. Chem. 267:13585-13592(1992).
                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-92317087; PubMed-1339433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE004778; AAG06957.1; -.
                      Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AA; 30486 MW;
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hes 15; Conserv
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SEQUENCE
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Spermatophyta, Nagnollophyta; sudiocryledons; corre endicots; rosids; cox and controlled to the control of the
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PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP; Complete proteome.
SEQUENCE 468 AA; 52234 MW; A4738F224237494E CRC64:

SKK

Length 468;

DB 1; 0.022;

Query Match

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0
                                                                                                                                                                                                                                                                                                                         Gaps
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Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;

"Genome-based analysis of virulence genes in a non-biofilm-forming

Staphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:1577-1533 (2003).

-!- CATALXTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose

S-phosphate + CO(2) + NADPH.

-!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                  PROBABLE 3-HYDROXYISOBUTYRATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                       37.5%; Score 75; DB 1; Length 347; 39.5%; Pred. No. 0.016;
                                                                                                                                                    MITOCHONDRION (BY SIMILARITY)
                                                                      InterPro; IPROO2204; Jahydroxisobut dh.
PROSITE; PSO0895; 3 HYDROXISOBUT DH; 1.
FYPOThetical protein; Oxidoreductase; NAD; Mitochondrion;
Transit peptide.

MITOCHONDRION (BY SIMILARITY)

TRANSIT
                                                                                                                                                                                                                                                                                                                       10; Mismatches 13; Indels
                                                                                                                                                                                                 NAD (ADP PART) (POTENTIAL). BY SIMILARITY.
                                                                                                                                                                                                                                      -> F (IN REF. 2).
6ED2E87CC3DE191C CRC64;
                                                                                                                                                                                                                                                                                                                                                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                            41 GFIGLGNMGFRMVNNLIRAGYKVTVHDINRDVMKMFTE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GND OR SE1192.
Staphylococcus epidermidis.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
or send an email to license@isb-sib.ch
                               EMBL, AL080282; CAB45888.1; ALT SEQ.
EMBL; AL161554; CAB79093.1; ALT SEQ.
EMBL; AY086845; AAM63893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006184; 6Pcdom BS.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD MAD.
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InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00393, 6PGD; 1.
Pfam, PF03446; NAD binding 2; 1.
PRINTS, PR00076; 6FGDHDRGNASE.
TIGRFAMS; TIGR00873; 9nd; 1.
                                                                                                                                                                                                                                                      37364 MW;
                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                  219 2
21
347 AA;
                                                                                                                                                                                                                                                                                                     Local Similarity
tes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1282;
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Q8CP47;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang R.F., Khan A.A., Cao W.W., Cerniglia C.E.;
"Identification and sequencing of a cDNA encoding 6-phosphogluconate dehydrogenase from a fungus, Cunninghamella elegans and expression of the gene in Escherichia coli.";
FEMS Microbiol. Lett. 169:397-402(1998).
-:- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
6-PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
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                                13; Indels
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                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Zygomycota, Zygomycetes, Mucorales,
Cunninghamellaceae, Cunninghamella.
                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                       6 GVVGLAVMGKNLAWNIESRGYSVSVYNRSRQKTDEMVK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GLIGLAVMGQNLILNMNDHGFVVCAYNRTTSKVDDFL 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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37.5%; Score 75; DB 34.2%; Pred. No. 0.02; tive 12; Mismatches
                                                                                                                                                                                              485 AA
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Oxidoreductase; Pentose shunt; NADP.
SEQUENCE 485 AA; 53102 MW; F7E61
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006114; 6FGD_C.
InterPro; IPR006113; 6FGD_decarbox.
InterPro; IPR006115; 6FGD NBD.
InterPro; IPR006184; 6FGGOm_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 36112;
MEDLINE=99085678; PubMed=9868787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00393; 6PGD; 1.
Pfam, PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO0873; gnd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y17297; CAA76734.1; -. HSSP; P00349; 2PGD.
                  Best Local Similarity 34.2%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 37.8 ses 14; Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                  Cunninghamella elegans.
                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family.
                                                                                                                                                                                              CUNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                           060037;
                                                                                                                                                                              6PGD_CUNEL
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6PG9_ECOLI

RESULT 26

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                                                                                                                                                                                                                                                             "Genomic organization of the Klebsiella pneumoniae cps region responsible for serotype K2 capsular polysaccharide synthesis in the virulent strain Chedid.";
J. Bacteriol. 177:1788-1796 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson K., Selander R.K.;
"Intergeneric transfer and recombination of the 6-phosphogluconate dehydrogenase gene (gnd) in enteric bacteria.";
Proc. Natl. Acad. Sci. U.S.A. 91:10227-10231(1994).
---- CATALITIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                                                                                                                                                                        Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.0%; Score 74; DB 1; Length 468; 38.2%; Pred. No. 0.03; tive 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :|: :|| : |: |: |: |: | : | CVVGMAVMGRNLALNIESRGYTVSVFNRSREKTE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
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(Rel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D21242; BAA04786.1; -.
EMBL; U14471; AAC43817.1; -.
PIR; D56146; D56146.
HSSP; P00349; ZPGD.
INTERPO; IPR008927; GDGDH_C_like.
INTERPO; IPR006114; GPGD_C.
INTERPO; IPR006114; GPGD_C.
INTERPO; IPR006115; GPGD_decarbox.
INTERPO; IPR006115; GPGD_NAD.
INTERPO; IPR006115; GPGD_NAD.
INTERPO; IPR006118; GPGD_NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95024018; PubMed=7937867;
                                                                                                                                                                                                   MEDLINE=95204345; PubMed=7896702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
TIGRPAMS; TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 12-456 FROM N.A.
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                                            Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 13; Conserv
                                                                                                                                                         FROM N.A.
                                                                                                               NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CW 7380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _6PGD_SALTY
P14062;
01-JAN-1990 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 28
    4446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol, 176:3126-3139(1994).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Jayarathe P., Bronner D., Maclachlan R.P., Dodgson C., Kido N., Whitfield C.; "Cloning and analysis of duplicated rfbM and rfbK genes involved in the formation of GDP-mannose in Escherichia coli 09:K30 and participation of rfb genes in the synthesis of the group I K30
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
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PROSITE; PS00461; 6PGD; 1.

Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.
SEQUENCE 468 AA; 51625 MW; C13D94CFD78BFF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.0%; Score 74; DB 1; Length 468; 38.2%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :|::|| : |: |:||:||: | : | CVGMAVMGRNLALNIESRGYTVSVFNRSREKTE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P41576; Q48461;
01-NOV-1995 (Rel. 32, Created)
N-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                        468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.2%; Preu. ....
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InterPro; IPR006114; 6PGD.
InterPro; IPR006114; 6PGD.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_NAD.
InterPro; IPR006118; 6PGD_NAD.
InterPro; IPR006118; 6PGD_NAD.
InterPro; IPR006118; 6PGD_NAD.
PFam; PF003446; NAD binding 2; 1.
PFam; PF03446; NAD binding 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=09:K30:H12 / E69;
MEDLINE=94252978; PubMed=7515042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L27646; AAA21136.1; -. PIR; I41250; I41250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capsular polysaccharide."
J. Bacteriol, 176:3126-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 38.2
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                                                                                        STANDARD;
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                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
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ID 6PGD KLEPN
                                                                                        6PG9 ECOLI
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Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;

Complete proteome SEQUENCE 468 AA

N M M

28-FEB-2003 (Rel. 41, Last annotation update) 6-phosphogluconate dehydrogenase, decarboxylating (BC 1.1.1.44) GND OR STM2081.

STRAIN=LT2;

SEQUENCE

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Gaps

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Indels

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Insect Mol. Biol. 1:213-222(1993).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHMAX: Haxces monophosphate shunt.
-!- PATHMAX: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE=94093871; PubMed=8269100;
Scott M.J., Kriticou D., Robinson A.S.;
Isolation of cDNAs encoding 6-phosphogluconate dehydrogenase and glucose-6-phosphate dehydrogenase from the mediterranean fruit fly Ceratitis capitata: correlating genetic and physical maps of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ceratitis capitata (Mediterranean fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
                                                                         37.0%; Score 74; DB 1; Length 468; 38.2%; Pred. No. 0.03;
468 AA; 51395 MW; D8EBB53A2DAADBF7 CRC64;
                                                                                                                                                                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
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InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006116; 6PGD_NAD.
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Pfam; PP03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
TIGRFAMS; TICR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S67873; AAB29396.1; -. HSSP; P00349; 2PGD.
                                                       Query Match
Best Local Similarity 38.2<sup>3</sup>
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 38.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6PGD CERCA
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                                                                                                                                                                                                                                                                                                                                                                                             RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91260454; PubMed=1710759;
Jiang X.M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.;
"Structure and sequence of the rfb (O antigen) gene cluster of
Salmonella serovar typhimurium (strain LT2).";
Mol. Microbiol. 5:695-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose -S-phosphate + CO(2) + NADPH.
-!- PATHWAY: Haxcose monophosphate shunt.
-!- SATHWAY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                         Reeves P., Stevenson G., "Cloning and nucleotide sequence of the Salmonella typhimurium LT2 mind gand incleotide sequence of the corresponding sequence of Escherichia coli K12." Mol. Gen. Genet. 217:182-184(1989).
                                            Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBL_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dykhuizen D.E., Green L.;
Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOSTIER, POOSA9, LAND.

FINETPRO, IRRO08927; GDGDH_Clike.
INTERPRO; IRRO08927; GDGDH_Clike.
INTERPRO; IRRO06114; GPGD_C
INTERPRO; IRRO061114; GPGD_C
INTERPRO; IRRO061115; GPGD_MD.
INTERPRO; IRRO061115; GPGD_MD.
INTERPRO; IRRO06115; GPGD_MD.
PFAM: PPOO393; GPGD, 1.
PFAM: PPOO393; GPGD, 1.
PRONTS; PRO007; GPGDHDRGNAS.
IIGREAMS; TICRO0873; gnd; 1.
PROSITE; PSOO461; GPGD; 1.
                                                                                                                                                                                                                                                                        MEDLINE=89364685; PubMed=2671649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE008792; AAL20985.1; -.
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EMBL; M64332; AAA27137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X56793; CAA40131.1; -. PIR; S04397; S04397.
HSSP; P00349; 2PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-57 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
                      Salmonella typhimurium.
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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family

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.0%; Score 74; DB 1; Length 481; 38.9%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 AA; 52963 MW; FOABB506AD1B86D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LGLGLMGSGIVSNLLXMGHTVTVWNRTAEKCDLFIQ 38
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IPR008927; 6DGDH_C_like.

InterPro;

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RA MEDLINE=21849401; PLUBMEd=211853360;

RA MODLINE=21849401; PLUBMEd=211853360;

RA Good V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gonlins M., Connor R., Tronin A., Davis P., Fieltwell T., Fraser A.,

RA Gonles S., Goble A., Hamilan N., Harris D., Hidalgo J., Hodgeon G.,

RA James K., Jones J., Jones M., Leather S., McDonald S., McLean J.,

A James K., Onose L., Murghl L., Niblett D., Odell C.,

RA Joner K., O'Neil S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Coliver K., O'Neil S., Bearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Ratlon J., Simmonds M., Squares R., Squares S., Stevens K.,

Raplor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckært G., Aert R., Robben J., Grymonprez B.,

Woltjens I., Volckært G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Volckært G., Aert R., Robben J., Grymonprez B.,

Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Eger P., Zimmermann W., Wedler H., Wamulut R., Pennardt R., Pohl T.M.,

Eger P., Zimmermann W., Wedler H., Wamulut R., Pernelle B.,

Lucas M., Rochet W., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rochet W., Gaillardin C., Tallada V.A., Garzon A., Howeller J., Moreno S., Armstrong J., Potashkin J.,

Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

Nandre Sandre Sandre Schizosaccharomyces pombe.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 415:871-880(2002).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                             MELLINE-28162722; PubMed=9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                         6PGD_SCHPO STANDARD; PRT; 492 AA.
P78812; Q9UQWS;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 4). Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.11.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                      SPBC660.16.
Schlizosaccharomyces pombe (Fission yeast).
Eukaryota. Fungi, Ascomycota, Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNAs.";
DNA Res. 4:363-369(1997).
                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
                        GPGD_SCHPO
RESULT 30
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EMBL; D89161; BAA13823.1; ALT_INIT.

EMBL, AL034563; CAA22536'1; --PIR, T40628; T40628. HSSP; P00349; 2PGD. GeneDB SPombe; SPBC660.16; -.

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                                                                                                                                                                                                    Length 492;
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                                                                                                                                                          219 220 IA -> ST (IN REF. 1).
492 AA; 53679 MW; FS5F342957A9D3B1 CRC64;
                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                  37.0%; Score 74; DB 1;
37.8%; Pred. No. 0.031;
tive 7; Mismatches 1
                                                                                                                                                                                                                                                                                                                      Search completed: September 16, 2004, 07:46:09
Job time : 12 secs
        InterPro; IPR006183; 6PGD.—
InterPro; IPR006144; 6PGD.C.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_MAD.
InterPro; IPR0061184; 6PGdom_BS.
Pfam; PP00343; 6PGD; 1.
PRINTS; PR00076; 6PGDHDROMASE.
TIGREAMS; TIGR0083; gnd; 1.
                                                                                                                                                Oxidoreductase; Pentose shunt; NADP. CONFLICT 219 220 IA -> S'
                                                                                                                                                                                                                   Local Similarity 37.8
hes 14; Conservative
                                                                                                                                     PROSITE; PS00461; 6PGD; 1
                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                        Best Loca
Matches
δ
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Q88ue9 lactobacill
Q819e3 bacillus ce
Q911E8 pseudomonas
Q88nE2 pseudomonas
Q88nE2 pseudomonas
Q81935 bacillus an
Q98gh7 rhizobium 1
Q82mw0 streptomyce
Q812mw0 streptomyce
Q812mw0 streptomyce
Q812mw0 streptomyce
Q812mw0 streptomyce
Q82mw0 streptomyce
Q82ne arabidopsis
Q99gk1 xanthomonas
Q84my1 bordetella
Q93nE8 thizobium m
Q7wjp8 bordetella
Q830a7 enterococcu
Q8my1 bordetella
Q80dh xanthomonas
Q810a7 enterococcu
Q8my1 bordetella
Q80dh xanthomonas
Q810a7 enterococcu
Q8my2 thermoroga
Q910a streptomyce
Q131a2 staphylococ
Q9wy19 thermoroga
Q910a streptomyce
Q8my1 bradyrhizob
Q912d streptomyce
Q80dn bradyrhizob
Q912d listeria in
Q80x9 listeria mo
Q80x0 listeria mo
Q80x0 listeria mo
Q80x0 listeria mo
Q80x1 listeria mo
Q80x1 listeria mo
Q80x1 corymebacte
Q81x8 salmonella
Q81x8 salmonella
Q82x9 thermoromaer
Q81x8 salmonella
Q82x1 arabidopsis
Q82x1 salmonella
Q82x1 salmonella
Q82x1 salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9cdk4 Tactococcus
Q9c990 arabidopsis
Q8ubw3 agrobacteri
Q8Aq44 streptomyce
Q949m8 arabidopsis
Q88aS listeria mo
Q88xx1 encephalito
Q81f73 agrobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q875m5 Kluyvecromyc
Q87648 saccharomyc
Q97ze5 sulfolobus
Q97ze5 sulfolobus
Q8226 salmonella
Q81q70 oryza sativ
Q7vzx5 candidatus
Q87m3 anabaena sp
Q9ng70 leishmania
Q9ngr1 leishmania
Q9ngr1 leishmania
                                                                                                                                                                                                                   051509
099TY2
099TY2
099EX6
086E88
0981R3
089NU4
092D17
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QB23HB
QB2ALV4
QB3Q26
QB3Q26
QB3Q26
QB3D2
QB3D2
QB1D2
QB1AQ3
QB7AQ3
QB7A
           Q819E3
Q911R8
Q88NR2
                                           Q81S35
Q98GH7
                                                                                     Q7WFP7
Q7W489
Q9SZE1
                                                                                                                                Q930R8
Q7WJP8
                                                                                                                                                Q7WAJ7
Q8EDH8
Q830A7
Q8R8Q4
Q7U3K2
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Q92BX9
Q8Y7B0
Q8NKA5
                                                                                                                                                                                          Q8 PDM7
Q8 9 M84
                                                             Q82MW0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBSRX1
QBUF73
QB75M5
QB76H8
Q972E5
QBXBD4
QBXBD4
QBZ2T6
QBLQ70
QPLQ70
Q7VRX5
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Q9NGR1
Q95UN7
  16
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5
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886
886
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886
85
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82.5
82.5
82.5
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Q922p9 mus musculu Q9cyql mus musculu Q9cyql mus musculu Q9bxk2 homo sapien Q8t079 drosophila G94a74 arabidopsis Q94b07 arabidopsis Q91wp0 arabidopsis Q81wp0 arabidopsis Q81y7 oryza sativ Q97dx8 clostridium Q97xz7 sulfolobus Q92n92 thizobium m Q8tt25 methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9btil homo sapien
                                                   2004, 07:30:52 ; Search time 39 Seconds (without alignments) 307.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                     1017041
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                 of hits satisfying chosen parameters:
                                                                                                                                                  1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                      US-10-067-482-2_COPY_271_308
                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0922P9
09CYQ1
09CYQ1
09BT079
094A74
094B07
094B07
091B00
091B00
091NP0
091NP0
091NP0
091NP0
097XZ7
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_mhc:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 2000000000
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110
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                                                      September 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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Match
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10.
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Perfect score:
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1066
1126
1125
1123
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1123
1108
1108
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                                  OM protein
                                                                                                       Sequence:
                                                                                                                                                Searched:
                                                                                                                                                                                                                                              Database
                                                    Run on:
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RA Kawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawa J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., Rakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Ratto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ratto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radto T., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kadota K., Matsuda H., N., Nishio E., Kochiwa H., Rachima H., Ratiol D., Rochima H., Wagner L., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Rakai K., Okido T., Fletcher C., Flujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N., A Nordone P., Ring B., Ringald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1921272; Npac.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004616; F:phosphapluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006098; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                  MGD: MGI:1921272; Npac.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004616; F:phosphognonate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pencose-phosphate shunt; IEA.
GO; GO:0006098; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Mecazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.0%; Score 166; DB 11; Length 546; 100.0%; Pred. No. 4.3e-13;
                         Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006893; AAH06893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 AA; 59715 MW; F5D2090DE1F64723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                 InterPro; IPR006115; 6PGD NAD.
InterPro; IPR000637; AT hook.
InterPro; IPR000313; PWWP_domain.
                                                                                                                                                                                                                                                                                                                                          Pfam; PF02178; AT hook; 1.
Pfam; PF03446; NAD binding_2; 1.
Pfam; PF00855; PWWP; 1.
PROSTITE; PS50812; PWWP; 1.
SEQUENCE 546 AA; 59715 MW; FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK014456; BAB29363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25, 3930401K13R1k protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001)
EMBL; AK014456; BAB29363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPAC OR 393040IK13RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CYQ1
Q9CYQ1;
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0
                              P95165 mycobacteri
Q94ku2 spinacia ol
Q92paz rhizobium m
Q8fbg0 escherichia
Q8x37 brucella me
Q8fxg6 brucella su
Q92p61 rhizobium m
Q92qq2 pasteurella
Q7vmx4 haemophilus
Q87609 saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, BC003633; AA403,633.1.; —

EMBL, BC003634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005637; F:DNA binding; IEA.

GO; GO:000698; P:pentose-phosphate shunt; IEA.

GO; GO:000635; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:000635; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR006113; FWPP_domain.

Pfam; PF02178; AT hook; 1.

Pfam; PF03446; NAD binding_2; 1.

Pfam; PF03446; NAD binding_2; 1.

SMART; SM00384; AT hook; 1.

PROSITE; PS50812; PWWP; 1.
           mycobacteri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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              28vjv7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57215 MW; ED3E2853938A211F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 200; DB 4;
100.0%; Pred. No. 1.6e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similar to RIKEN cDNA 3930401K13 gene (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 AA
                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                 Q8YAX7
Q8FXG6
Q92P61
                                                                                                                                                                                                                                Q9CKQ2
O7VMX4
                                          P95165
Q94KU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                               292PA2
                                                                                                                        Q8FBG0
              CVUV8C
                                                                                                                                                                                                                                                                                     0876H9
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
RIKEN CDNA 3930401KL3 gene.
NPAC OR 3930401KL3 gene.
                   16
116
116
116
116
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nes 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 AA;
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                40.0
40.0
40.0
339.8
339.5
339.5
339.5
339.5
339.5
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80
79.5
79
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79
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Q922P9 Q922P9

RESULT 2 Q922P9

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Matches

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Gaps

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09BTI1;

O9BTI1

RESULT 1 Q9BTI1

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Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                              SEQUENCE FROM N.A.
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                                SEQUENCE FROM N.A.
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004616; F:DNA binding; IEA.
GO; GO:0006098; P:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
InterPro; IPR006115; GOD NAD.
InterPro; IPR006115; GOD NAD.
InterPro; IPR00637; AT hook.
InterPro; IPR000313; PWWP_domain.
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                          Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                           New L., Han J.;
"A novel cytokine-like nuclear factor, n-pac.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF326966; AAK15524.1;
                                                                                    59744 MW; B3AC1562477ABC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59827 MW; C7D785CCBF83204A CRC64;
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 166; DB 4; I
Pred. No. 4.3e-13;
                                                                                                         Score 166; DB 11;
Pred. No. 4.3e-13;
                                                                                                                                                                         270 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                 83.0%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                    1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                               547 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LD22344p (CG4747-PA).
BEST:LD22483 OR BEST:LD29743 OR CG4747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                  Cytokine-like nuclear factor n-pac.
Homo sapiens (Human).
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR000637; AT hook.
InterPro; IPR000313; PWWP_domain.
                             Pfam; PF02178; AT hook; 1.
Pfam; PF03446; NAD binding 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02178; AT hook; 1.
Pfam; PF03446; NAD binding 2; 1.
                                                 Pfam; PF00855; PWWP; 1.
SMART; SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
SEQUENCE 546 AA; 59744 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00855; PWWP; 1.
SMART; SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24,
                                                                                                         Query Match
Best Local Similarity 100.
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8T079; Q9VL51;
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                                                                                                                                                                                                                             Q9BXK2
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                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                                                                    Q9BXK2
 ID DATE DATE OF CO.
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RAMEDLINE-20196006; PubMed=10731132;
RADAGRAME N. Celniker S.E., Holt R.A., Evens C.A., Gocayne J.D., Addams M.D., Celniker S.E., Il P.W., Hoskins R.A., Galle R.F., Garlen G. S., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortnam J.R., Yandell M.D., Zhang Q., Chen L.X.,
RAD Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RAD Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RAD Ballew R.M., Basun J.R., Nandell M.D., Baytaktaroglu L., Beasley E.M.,
RAD Ballew R.M., Basun D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAD Ballew R.M., Basun D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAD Ballew R.M., Basun D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAD Ballew R.M., Basun D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAD Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAD Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAD Burtis K.C., Busam D.A., Butler M., Dugan-Rocha S., Plunkov S.,
RAD Burtis K.C., Busam D.A., Butler M., Dugan-Rocha S., Plunkov B.C., Dunn P.,
RAD Burtis K.J., Evangelista C.C., Ferraz C., Ferriera S., Plukov B.C., Dunn P.,
RAD Burtis N.J., Harvap D., Heiman T.J., Hermandez J.R., Houck J.,
ROGER K., Goorfell J.H., Gu Z., Kennison J.K., Ketchum R.A., Jalali M., Kalush F., Karfet C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lai Y., Lewitsky A.A., Li J., Li Z., Ling Y., Lin X.,
Allali M., Kalush F., Karfet G., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Lewitsky A.A., Li J., Mei M., McCheod M.P., McCheod
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STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY069497; AAL39642.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2185-2195(2000)
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FROM
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                                                                                                                                                                                           enzyme.";
Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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EMBL; AE003627; AAF52846.3; -.
FlyBase; FB900043466; BEST:LD22483.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
InterPro; IRRO06115; 6F9ED NAD.
InterPro; IRRO06115; 6F9ED NAD.
Pfam; PF03446; NAD binding_2; 1.
Pfam; PF03446; NAD binding_2; 1.
PROSITE; SMO0293; PWWP; 1.
PROSITE; PS50812; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,

Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Hayashizaki Y.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Karlii-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0008442; F:3-hydroxylsobutyrate dehydrogenase activity; IEA. GO; GO:0004616; F:3-hydroxylsobutyrate dehydrogenase (decarboxyla. . .; GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; GO; GO:0006098; P:pettose-phosphate shunt; IEA. GO; GO:0006073; P:valine metabolism; IEA. Interpro; IPR002204; 3hydroxisobut_dh. IEA. Interpro; IPR006118; GPGD NAD. Pfam; PF03446; NAD_binding_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248;
                                                                                                                                                                            Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Arabidopsis cDNA clones.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY049298; AAK83640.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00076; 6PGDHDRGNASE.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SEQUENCE 248 AA; 26336 MW; C96912B3E2A7E677 CRC64;
                                                                                                                                               602 AA; 65252 MW; E004EEC610C23625 CRC64;
                                                                                                                                                                                                                                                      319 GFLGLGMMGSTIVKDLIYTGHKVVVWNRTIDKCQPFAE 356
                                                                                                                                                                                                                                                                                                                                                                   (Tremblrel. 19, Created)
(Tremblrel. 19, Last sequence update)
(Tremblrel. 24, Last annotation update)
                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVE 41
                                                                                                                                                                            Score 126; DB 5;
Pred. No. 7.4e-08;
5; Mismatches 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 125; DB 10;
Pred. No. 3.9e-08;
                                                                                                                                                                                                                                                                                                                                         248 AA
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Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q94B07;
01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                          63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.5
Best Local Similarity 60.5
Matches 23; Conservative
                                                                                                                                                                                         Local Similarity 60.5
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ecker J.R.;
                                                                                                                                               SEQUENCE
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                        Q94A74;
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                                                                                                                                                                                                                                                                                                                                          Q94A74
                                                                                                                                                                                                         Matches
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EMBL; AY044183; AAK94781.1; EMBL; AY044183; EMBL; EM
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BNBL; AB025639; BAB01322.1; -.

GO; GO:0006442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO; GO:00064616; F:3-hosphogluconate dehydrogenase (decarboxyla. . .; IEA.

GO; GO:0006098; P:pentose-phosphate shunt; IEA.

GO; GO:0006573; P:valine metabolism; IEA.

InterPro; IPR002204; 3hydroxisobut_dh.

InterPro; IPR006183; 6FGD.
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Gamma hydroxybutyrate dehydrogenase (EC 1.1.1.61).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eutosids II; Brassicales, Brassicaceae, Arabidopsis.
NCBI TaxID=3702;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Breitkreuz K.B., Van Cauwenberghe O.R., Allen W.L., Jakobs C.,
Talibi D., McLean M.D., Andre B., Shelp B.J.;
"Plant gamma-hydroxybutyrate dehydrogense, a novel fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 3. I. Se features of the regions of 4,504,864 bp covered by sixty Pl and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 AA; 30678 MW; 3E6715DFF96593D6 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%; Score 125; DB 10;
60.5%; Pred. No. 4.5e-08;
iive 4; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
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es 23; Conserv
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Gaps

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Indels

8;

Mismatches

4;

34

88

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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD
                                            55 GFLGMGIMGSPMAQNLIKAGCDVTVWNRTKSKCD
 22; Conservative
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                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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01-OCT-2000
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                                                                                                                               O9LNPO
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Q8LQJ7
Matches
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EMBL; AY085690; AAM62909.1; -.
EMBL; BT008734; AAP42747.1; -.
EMBL; BT0080734; AAP42747.1; -.
EQ; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO: GO:0006098; P:pentose-phosphate shunt; IEA.
InterPro; IPR006115; 6PGD_NAD.
Pfam; PF03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sakurai K., Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yaun S., Shinozaki K., Davis R.W., Theologis A., Bcker J.R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawi J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakuraf T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
                                                                                                                0
                                                                                  62.5%; Score 125; DB 10; Length 289; 60.5%; Pred. No. 4.5e-08; tive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haās B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          젎
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Stefdmann K., Frantl-Length CDNA from Arabidopsis thaliana."; Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
             Pfam, PF03446; NAD binding 2; 1.
PRINTS, PR00076; &FCDHDRGNAGE.
PROSITE; PS00985; 3 HYDROXXISOBUT DH; 1.
SEQUENCE 289 AA; 30691 MW; 3E67002A19706636 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36287 MW; D012C16284C5FA52 CRC64;
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                           38
                                                                                                                                                           GFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVE 41
                                                                                                                                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                                                                                            343 AA.
                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Hypothetical protein (At1g17650).
                                                                                                                                                                                                                                            PRT;
InterPro; IPR006115; 6PGD NAD
                                                                     Query Match
Best Local Similarity 60.5*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 0:0-0(2002).
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Length 343;

Score 123; DB 10; Pred. No. 9.9e-08;

61.5%; 64.7%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mnkharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Arabidopsis thaliana BAC F1L3 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.1e-07;
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     387
                                                                                                                                                                                                                                                   F1L3.35.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                       Created)
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     PRT;
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                                                                                             (TrEMBLrel. 15, (TrEMBLrel. 15,
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22,
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ecker J.R.;
Submitted (FEB-2000)
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Submitted (APR-2000)
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01-OCT-2002 (
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us-10-067-482-2 copy 271 308.rspt

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Pfam; PF03446; NAD binding 2; 1.
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NCBI_TaxID=2287;
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                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .; IEA.
                                                                                                                                                                                                   STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Nipponbare;
Cooper B., Hutchison D., Park S., Guimil S., Luginbuhl P., Ellero C.,
Goff S., Glazebrook J.;
"Identification of Rice (Oryza sativa) Proteins Linked to the Cyclin-
Mediated Regulation of the Cell Cycle.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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EMBL; A224558; AAO72678.1; - EMBL; AB110167; BAC78559.1; - GO; GO:0004442; F:3-hydroxyiscbutyrate dehydrogenase activity; IEA. GO; GO:000646; F:phosphogluconate dehydrogenase (decarboxyla. .; GO; GO:0006599; P:pentose-phosphate shunt; IEA.
                                       Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein).
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeee, Oryza.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gamma hydroxybutyrate dehydrogenase-like protein (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                 clone:B1151A10.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003413; BAB91904.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFam; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SEQUENCE 343 AA; 35481 MW; 195ABBEDA048F84D CRC64;
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64.7%; Pred. No. 1.8e-07;
iive 4; Mismatches 8;
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gamma hydroxybutyrate dehydrogenase
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InterPro; IPR006115; 6PGD_NAD.
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InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD_NAD.
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Matches 22, Conservative
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                                                                                                                                    NCBI_TaxID=39947;
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                         B1151A10.17
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1D 084VC
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90) G0:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. G0; G0:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. InterPro; IPR006183; GFGD.
InterPro; IPR006183; GFGD.
InterPro; IPR006183; GFGD.
InterPro; IPR006184; GFGD.
InterPro; IPR00418; GFGD.
Individual Companies of Comp
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MEDLINB=2139325; PubMed=11466286;

MEDLINB=2139325; PubMed=11466286;

MEDLINB=2139325; PubMed=11466286;

MEDLINB=2139325; PubMed=11466286;

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838 (2001).

EMBL; AE007831; AAK81274.1;
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                           Length 293;
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PRINTS; PR00076; 6FGDHDRGNĀSE.
PROSTITS; PS00895; 3 HYDROXXISOBUT_DH; 1.
Hypothetical protein.
SEQUENCE 293 AA; 30496 MW; 2362B7AC4EE52038 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                           59.0%; Score 118; DB 10;
63.6%; Pred. No. 3.7e-07;
live 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GFLGLGIMGKAMAANLLRHGFRVTVWNRTLSKC 36
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                                                                                                                                                                                                                                                                                                                 Local Similarity 63.6
ses 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Gaps

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SEQUENCE FROM N.A.

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SEQUENCE TRAIN-C23 S1955 / DSM 2834;

MEDLINE=21929760; PubMed=11932384;

MEDLINE=21929760; PubMed=11932384;

MEDLINE=21929760; PubMed=11932384;

MATICAL N. Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A Allen N., Naylor J., Stange-Thomann N., DeArellanon K., Johnson R.,

A Linton L., McEwan P., McKernan K., Tarrell A., Ye W.,

A Linton L., McEwan P., McKernan K., Tarrell A., Ye W.,

A Linton L., McEwan P., McKernan C., Karrycki J.A.,

A Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

A Beigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Repry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Retcalf W.W., Birren B.;

R The genome of Methanosacian acetivorans reveals extensive metabolic
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO; GO:0006098; P:pentose-phosphate shunt; IEA. InterPro; IRR06115; 6FGD NAD. Pfam; PFO3446; NAD binding_2; 1. Complete proteome.

SEQUENCE 155 AA; 16030 MW; 7FB9B77D3CC771A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AR010722; AAM04058.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
                                                                                                                                                   Length 155;
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                                                                                                                                                                                              9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Euryarchaeota orders incertae
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                   Score 105; DB 16;
Pred. No. 9.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 17;
Pred. No. 6.2e-05;
5; Mismatches 13;
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InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD NAD.
                                                                                                                                                                                                                                                                                 LGLGAMGTALARTLLKNGHTVTVWNRTRSRAE 38
                                                                                                                                                                                                                                        3 LGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                            300 AA.
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                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-hydroxyisobutyrate dehydrogenase MA0614.
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                                                                                                                                                   52.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanosarcina acetivorans.
                                                                                                                             Query Match
Best Local Similarity 59.47
Fig. 2008 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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01-JUN-2003
01-OCT-2003
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Q88UE9;
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                                                                                                                                                                                                                                                                                                                  GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:000856; F:nucleic acid binding; IEA.
GO; GO:0008616; F:nucleic acid binding; IEA.
GO; GO:00066098; P:pentose-phosphate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006598; P:pentose-phosphate shunt; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR002204; 3hydroxisobut_dh.
                                                                     She Q., Singh R.K., Confaloneri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
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Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Last annotation update)
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Pred. No. 7.3e-06;
7; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 AA.
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Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0076; GPGDHDRGNASE.
PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-UUN-2003 (TrEMBLrel. 24, Last ann
Putative oxidoreductase protein.
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                                      STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006115; 6PGD NAD.
InterPro; IPR000504; RNA rec mot.
Pfam; PF03446; NAD_binding 2; 1.
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58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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                 SEQUENCE FROM N.A.
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292 AA; 31987 MW; 8B04FC5E59A93423 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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                                                                                                  Local Similarity
nes 18; Conser
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                                                                                                                                                                                                                                                                                                                                           Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Filers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., M. Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., M. Bron P.A.,
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Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
EMBL; AL935559; CAD64827.1;
GO; GO:0004420; F:3-hydroxymethylglutaryl-CoA reductase (NADPH). .; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
GO; GO:0009058; P:biosynthesis, IEA.
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IVANDOVA N., SOROKIN A., Anderson I., Galleron N., Candelon B.,
IVANDOVA N., Sorokin A., Anderson I., Galleron M., Lapidus A.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
"Genome sequence of Bacillus cereus and comparative analysis with
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                                      HIBD OR LP 2548.
Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacceria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Complete proteome.
SEQUENCE 286 AA; 30351 MW; AC9E968BD5C222FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31).
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       3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016491; F:oxidoreductase activity; ile CO; GO:0004616; F:phosphogluconate dehydroget GO; GO:0005088; P:biosynthesis; IEA CO; GO:0006098; P:pentose-phosphate shunt; Il InterPro; IRROf6115; FGD NAD.
InterPro; IRROf6115; FGD NAD.
InterPro; IRROf6115; FGD NAD.
IRROFACE, IRROGACOA_red.
Ffam; PRO3446; NAD_binding_2; I: PROSITE; PS00066; HMG COA_REDUCTASE_I; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD NAD.
Pfam; PP03446; NAD binding 2; 1
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 48.6
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus anthracis.";
Nature 423:87-91(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 AA;
                                                                                                                                                                                   NCBI_TaxID=1590;
                                                                                                                                            Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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2019E3
1D Q019E3
AC Q019E
AC Q019E
AC Q019E
DT O1-OU
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Matches
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltery L., Tolentino E., Weekbrock-Wadman S., Yuan Y., Smith K.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";
Nature 406:959-964(2000).
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MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRID. D83371; D83371.
GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
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Pseudomonadaceae; Pseudomonas.
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   Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 AA; 30886 MW; F379B9582ACF81B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                          3-hydroxyisobutyrate dehydrogenase family protein
Score 99; DB 16;
Pred. No. 0.00011;
9; Mismatches 11;
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49.0%; Score 98; DB 16;
Best Local Similarity 52.9%; Pred. No. 0.00015;
Matches 18; Conservative 7; Mismatches 9;
                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GFLGLGGMGAAMATRLVQAGLEVTVWNRSAAACE 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonadaceae; Pseudomonas
   49.5%;
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EMBL, AP003001; BAB50239.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22608414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okted O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy K.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.H.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., Mitte O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama C., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.0%; Score 96; DB 16; Length 317; 51.4%; Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                               Dehydrogenase, putative.
BA1842.
Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AA; 33312 MW; CEA29415E4EF7A81 CRC64;
                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium loti (Mesorhizobium loti).
                                                               Created)
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      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE017029; AAP25747.1; -. TIGR; BA1842; -.
                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                        01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           closely related bacteria.";
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DNA Res. 7:331-338(2000).
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nes 18; Conservative
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 423:81-86(2003).
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M.;
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                                    281835;
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Q98GH7
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                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).

EMBL; ARO16778; ARN66768.1; -...

TIGR; PP1143; -...

ANN66768.1; -...

TIGR; PP1143; -...

TIGR; PP1143; -...

TIGR; PP1145; -...

TIGR;
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DNA Res. 9:189-197(2002).
EMBL; APO05957; BAC513951; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
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Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
48.0%; Score 96; DB 16; Length 295;
Best Local Similarity 51.5%; Pred. No. 0.00027;
Matches 17; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Pred. No. 0.00029;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 AA; 30664 MW; 27E6E003D82ED459 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 GFAGIGLMGLPMCRRLLAAGYPLTVWNRSPDKC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.0%; Sco. No. 0...
56.2%; Pred. No. 0...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 GYLGLGLMGTPMTRRLLKAGYQVSVWNRSEGK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03446; NAD binding 2; 1. PRINTS; PR00076; 6PGDHDRGNASE.
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InterPro; IPR006115; 6PGD_NAD.
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Best Local Similarity 56.2
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                Fraser
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RESULT 21

RESULT 22 Q81535

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STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
A Kawarabayasi Y. Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
The entire genomic sequence of Corynebacterium efficiens YS-314.";
The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AP00519; BAC18398.1;
EMBL, AP00519; BAC18398.1;
EMBL, AP00519; PR006183; GGDH C_like.

InterPro; IPR006183; GGDH C_like.

InterPro; IPR006184; GFGD C_like.

InterPro; IPR006184; GFGD MBS.

InterPro; IPR006113; GFGD MBD.

InterPro; IPR006113; GFGD MAD.

R InterPro; IPR006113; GFGD NAD.

R Ffam; PF03193; GFGD, NAD.

R Ffam; PF03194; NAD binding 2; I.

R PRINTS; PR00705; GFGDHDRGNĀSE.
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Fajardo-Cavazos P., Salazar C., Nicholson W.L.;
"Molecular cloning and characterization of the Bacillus subtilis spore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98015408; PubMed=9353924; Mueller J., Schiel S., Ordal G.W., Saxild H.H.; Mueller J., Schiel S., Ordal G.W., Saxild H.H.; Phroteional and genetic characterization of mcpC, which encodes a third methyl accepting chemotaxis protein in Bacillus subtilis."; Microbiology 143:3231-3240(1997).
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0
                                                                                                                                                                                                          Bacieria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490 AA; 53121 MW; BA20D7E0CDDB6761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative 6-phospho-gluconate dehydrogenase (Fragment).
                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 GVVGLAVMGSNLARNFARNGHTVAVYNRSTDKTDKLI
                                           490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                  Putative 6-phosphogluconate dehydrogenase,
                                                                                  Created)
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                                           PRT;
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                                                                              01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                         Corynebacterium efficiens.
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PROSITE; PS00461; 6PGD; 1.
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                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                    NCBI_TaxID=152794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                         Q8FTI1
Q8FTI1;
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RESULT 25
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                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
BMBL; ABO05027; BAC69253.1; -.
GO; GO:0004616; F:phosphoglucomate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MA-488 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 296;
                                                                                                                                                                                                                                                                                             Length 475;
                                                                                                                                                                                                                                                                                                                                    13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MA-4680 / AICC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                    475 AA; 50478 MW; DDCD80AE38E22DEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 AA; 30626 MW; 4A235B663CE97764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                    1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
Local Similarity 50.0%; Pred. No. 0.00067; les 16; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                         ch 48.0%; Score 96; DB 16;
1. Similarity 42.1%; Pred. No. 0.00045;
16; Conservative 9; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LGTGIMGAAMARNLARAGHTVRAWNRTRAKAE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 AA
                 InterPro; IPR006183; 6PGD.—
InterPro; IPR006184; 6FGGom BS.
InterPro; IPR006114; 6FGG C.
InterPro; IPR006113; 6PGD Gearbox.
InterPro; IPR006113; 6PGD Gearbox.
InterPro; IPR006115; 6FGD MAD.
Fram; PF003446; NAD binding 2; PRAMYE; PR00076; 6FGDHDKGNASE.
TIGRFAMS; TIGR00833; gnd; 1.
PRNSTE; PS00461; 6FGDHDKGNASE.
COMPIETE; PS00461; 6FGDH C.
SEQUENCE 475 AA; 50478 WW; DDCD80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
eDGDH_C_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative dehydrogenase
  InterPro; IPR008927;
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Matches
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STRAIN=12822 / ATCC BAA-587;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MARTIS D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cardeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Chillingworth T., Collins M., Cronin A., Davis P., Dogget J.,

R Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Ruter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

Winnin L., Whitehead S., Barrell B.G., Maskell D.J.;

M. "Comparative analysis of the genome sequences of Bordetella pertussis,

M. "Anderella parapertussis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G.,
                                                                                        Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 AA; 31371 MW; B9696B7BAD09CA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative oxidoreductase.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 92; DB 16;
Pred. No. 0.00092;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation up
Hypothetical protein (Putative dehydrogenase)
19915-150 OR AT4629120.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 35:32-40(2003).
EMBL; BX640434; CAE39062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.0%;
58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Juery Match
Bost Local Similarity 58.1.,
Best Local 18; Conservative
                                                                                          Bacteria; Proteobacteria; B
Alcaligenaceae; Bordetella.
                                                                  Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEOUENCE FROM N.A.
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                                                                                                                                                                                  SEQUENCE FROM N.A.
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M. MEDLINE=22827954; PubMed=12910271;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A cerdeno-Tarraga A. M., Temple L., James K., Harris B., Quail M.A.,

A cerdeno-Tarraga A. M., Temple L., James K., Harris B., Quail M.A.,

A chtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Cerdeno-Tarraga A. M., Callins M., Choil A., Davis P., Doggett J.,

A chtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A chtman T., Goble A., Hamlin M., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

R. Rabbinowlitsch B., Rutter S., Sanders B., Seeger K.,

R. Rharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

M. Whitehead S., Barrell B.G., Maskell D.J.;

RT Bordetella parapertussis and Bordetella bronchiseptica.",

REDI, BK640449; CAB34588.1; -.
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                                                                                                               . .; IEA.
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                                                                                        GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .;
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6PGD_NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
photoproduct lyase (spl) gene, which is involved in repair of radiation-induced DNA damage during spore germination.";
J. Bacteriol. 175:1735-1744 (1993).
EMBL: X97385; CAA66053.1; -.
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                                                                                                                                                                                                                                                                                                                     Score 92; DB 2; Length 43;
Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AA; 31326 MW; 91AC4FBF73F6925F CRC64;
                                                                                                                                                                                                                                                                                                  43 AA; 4797 MW; 4E9F29CDCB64945B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AA.
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                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                             Pfam; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                               46.0%;
                                                                                                                                                                                                                                                                                                                                                                       53.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenaceae, Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RB50 / ATCC BAA-588;
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 53.13
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
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Best Loca Matches

RESULT 28

Q7W489

Q7WFP7

RESULT 27

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Gaps

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                                                                                                                                                                                                                                                                                                                                          Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Sekim M., Shinn P., Southwick A., Shinnezaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene AT4929120 (GI:7269810)."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-22022145; PubMed=12024217;
da Silva A.C.R., Ferro U.A., Reinach F.C., Farah C.S., Furlan L.R.,
duaggio R.B., Monterico-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Camarotte G., Cannaravan F., Cardozo O., Chambergo F., Ciaphina L.P.,
Cicarelli R.M.B., Coutthho L.L., Cursino-Santos J.R., Fl-Dorry H.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Formighheri B.F., Franco M.C., Grabez A.,
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas axonopodis (pv. citri).
Bacteria, Forteobacteria; Gammaproteobacteria, Xanthomonadaceae;
Xanthomonadaceae; Xanthomonas.
VCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 protein.
334 AA; 35371 MV; EC0038096DB836BA CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Dehydrogenase.
XAC0322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR, T08967; T08967.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0006098; P:pentose-phosphate shunt; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR002227; TY005inase.
Pfam; PF03446; NAD binding 2: 1
PRINTS; PR00076; 6PGDHDRGNASE.
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EMBL; AY062952; AAL33784.1; -.
PIR; T08967; T08967.
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Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                         Nature 417:459-463 (2002).

EMBL; AR011657; AAM35214.1; -.

G0; G0:008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

G0; G0:0006573; P:valine metabolism; IEA.

InterPro; IPR002204; 3hydroxisobut dh.

PR0571E; PS00895; 3_HYDROXYISOBUT_BH; 1.
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                                                                                                                                                                                                                                                                                                                    292 AA; 30453 MW; 4344A00544D44B8B CRC64;
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Job time : 43 secs

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Aaw69240 Clone
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Aau21690 N
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Adc46454
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Aae19927
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                      1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 100 summaries
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                             OM protein - protein search, using sw model
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AAU20515
AAU20515
AAU2051813
ADC46454
AAW09404
ABW09982
AAU20553
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AAU21590
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AAU21690
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AAE19927
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AAE36392
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AAB19491
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AAG10424
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                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                             1 MAAVSLRLGDLVWGKLGRYP.
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11: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp201s:*
                                                                                                                                                                                                                                                                      geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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length: 2000000000
                                                                              US-10-067-482-2
2866
                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                             seq
                                                                                      Perfect score:
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Maximum DB
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9926 CO: 1222 Arc 9956 Arc 9954 Arc 1159 Br. 1159 Br. 1223 Arc 1223 Arc 1223 Arc 1224 Arc 1224 Arc 1227 Arc 122	Adu29967 Protein e Adu29967 Protein e Adu3283 Protein e Abu3123 Protein e Abu3123 Protein e Abu37446 Neisseria Aay7446 Neisseria Aay7446 Neisseria Aay7446 Neisseria Aay7446 Protein e Abu1706 Protein e Abu3837 Protein e Abu3835 Protein e Abu39551 Protein e Abu47003 Protein e Abu47003 Protein e Abu47004 Arabidops Add33520 Alcaligen Abu4756 Protein e Abu4756 Protein e Abu4756 Protein e Abu4756 Protein e Abu4759 Protein e Abu476463 Arabidops Add36852 Acinetoba Add3681 Arabidops Arabidops Arabidops Arabidops Arabidops Arabidops Arabidops Arabidops Arabidops Arabid	3374 Human 3521 Human
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Gaps

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Indels

09 09 120

120

240 240 300

180 180

AA016415

us-10-067-482-2.rag

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Secreted protein; nutritional source; cell proliferation activity; cell differentiation activity; immune stimulant; tissue growth activator; haematopoiesis regulator; anti-inflammatory; tumour invasion suppressor; tumour inhibitor; clone AQ73_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ICEBETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKWGHTVTVWNRTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM 420
                                                                                                                                                                                                                                                                                                                                                                          61 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP
                                                                                                                                                                                                                                                                                                  121 NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ICEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 GKTSFFLGEVGNAARAMLIVNAVQGSFMATIAEGLTLAQVTGQSQQTLLDILAQGLASI
                                                                                                                                                                                                                                                            121 NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPFKDEKD
                                                                                                                                                                                                    1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVBQL
                                                                                                                               1 MAAVSLRIGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
      Score 2858; DB 6;
Pred. No. 2.7e-254;
                                                 0; Mismatches
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                                 Local Similarity 99.8
hes 552; Conservative
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                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee SY;
Y;
                                                                                                                                                                                                                                                                                                                                                                              cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS; cancer; developmental disorder; renal tubular acidosis; anaemia; asthma; mental retardation; neurological disorder; Alzheimer's disease; epilepsy; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; Crohn's disease; transgenic animal; animal model.
Aab 92800 Human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid-associated proteins and polynucleotides, useful for diagnosing, treating or preventing cell proliferative (e.g. cancer), neurological (e.g. epilepsy or Parkinson's disease), or autoimmune disorders (e.g. AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM; Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IJ; Ramktumar J, Griffin JA, Yang J, Sanjanwala MW, Baughn MR; Borowsky ML, Yao MG, Wallan NK, Bandman O, Lal PG, Becha SD, Richardson TW, Elliott VS, Luo W, Tang YT, Zebarjadian Y, Lu
                                                                                                                                                                                                                                                                                                                                                                 nucleic acid-associated protein; NAAP; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                      Human nucleic acid-associated protein (NAAP) - SEQ ID No 12
                                                                                       ALIGNMENTS
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  AAB70073
AAB92800
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29-JUN-2001; 2001US-0301787P.
29-JUN-2001; 2001US-0301892P.
29-JUN-2001; 2001US-0301892P.
29-JUN-2001; 2001US-0301893P.
6-JUL-2001; 2001US-0303402P.
06-JUL-2001; 2001US-0303442P.
15-MAR-2002; 2002US-0364438P.
                                                                                                                                                                                                AA016415 standard; protein; 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2002; 2002WO-US021179
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, Elliott VS,
    4 4
                                                                                                                                                                                                                                                                                     (first entry)
    203
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    6.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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96US-00766263. 97US-00989232.

13-DEC-1996; 11-DEC-1997;

associated protein of the invention

Sequence 553

(GEMY) GENETICS INST INC.

480 480 540 540

420

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ICEBETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |-----EGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is secreted protein, encoded by a polynucleotide of the invention. The DNA was isolated from a human adult ovary CDNA library, and is designated clone AQ73 3. The DNA sequences and encoded polypeptides can be used as Tutritional sources or supplements, or may exhibit e.g. cytokine and call proliferation/differentiation activity, human stimulating or suppressing activity, haematopoiesis regulating activity, receptor/ligand activity, anti-inflammatory activity, activity, call activity, chambin activity, chemostatic/chemokinetic activity, cadherin/tumour invasion suppressor activity, tissue growth activity, tumour inhibition activity or other activities
                                                                                                             New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPYHAHKEEMIKINKGKRFQQAVDAVEBFLRRAKGKDQTSSHNSSDDKNRNSSEERSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAVSIRIGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 547;
                        Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 5.8e-250;
0; Mismatches 1;
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                      Racie
                                                                                                                                                               Claim 15; Page 66-67; 108pp; English.
                  Lavallie ER,
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                                  V, Agostino MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 546; Conservative
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                  Mccoy JM,
                                                                  WPI; 1998-362424/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                              N-PSDB; AAV44859
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 547 AA;
                              Spaulding
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Human cDNA clones represented in AAF98174 - AAF98489 encode secreted proteins AAB90567 - AAB90750. The CDNA clones are isolated from various clisue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The CDNA proteins and call proliferation/differentiation activity and may also be cyckine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences proteins, their agonists and/or antagonists exhibit haematopoiesis cemperatic/demokinetic activity; activity; activity, haematopoiesis activity; ceceptor/ligand activity; anti-inflammatory activity, haematopoiesis activity; and-or tumour inhibition activity; and-or tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490 can appear and activity activity activity and activity activity activity and activity activit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein, nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; haematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids encoding polypeptides, useful for modulating e cytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity.
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Pred. No. 5.8e-250;
0; Mismatches 1; Indels
                                                                                                                       Human AQ73_3 protein sequence SEQ ID 137.
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98.7%;
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Merberg D,
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         ICEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGGMGSGIVSNLLKAMGHTVTVWNRTA 300
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                                                                                               STVDADIVITELAQVIVSRGGRRILEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM 420
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                                                                                                                                                                                     PLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPWAAAANEVYKRAKALDQS
                                                                                                                                                                                                 475 FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTFWAAAANEVYKRAKALDQS
                                                    Novel human neoplastic disease associated polypeptide #123
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24 - FEB - 2000; 2000US - 0180628F.
24 - FEB - 2000; 2000US - 0180628F.
16 - MAR - 2000; 2000US - 018930P.
16 - MAR - 2000; 2000US - 019937F.
17 - MAR - 2000; 2000US - 019076F.
18 - AFR - 2000; 2000US - 019123F.
19 - MAY - 2000; 2000US - 0219123F.
19 - MAY - 2000; 2000US - 0219125F.
07 - JUN - 2000; 2000US - 021688F.
28 - JUN - 2000; 2000US - 021688F.
11 - JUL - 2000; 2000US - 021688 P.
11 - JUL - 2000; 2000US - 021748 F.
11 - JUL - 2000; 2000US - 0217496F.
11 - JUL - 2000; 2000US - 0217496F.
14 - JUL - 2000; 2000US - 0220964F.
14 - JUL - 2000; 2000US - 0224518F.
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01-DEC-2000;
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Barash SC, Rosen CA,

2001-465558/50 N-PSDB; AAS34889

diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis Novel polypeptides and polynucleotides useful as diagnostic reagents to

Claim 11; SEQ ID NO 417; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34057-AAS35050) and DNA conserved by the sequences encoding for these polypeptides. The sequences of the invention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative consortant in the diagnosis, treatment, prevention and/or prognosis of disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem consortant inver cancer, childhood cerebellar astrocytoma, or Hoddkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system clisorders, muscular disorders, reproductive disorders, immune system disorders, pulmonary disorders, reproductive disorders and renal clisorders. The polynuclectide sequences of the invention are also useful consorted therapy. AAUS1568-AAU21851 represent the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data obtained in electronic format directly from WIPO at

Sequence 550 AA;

US2003082758-A1.

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                                                                                                                   64 HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSG 123
                                                                                                                                                                              DEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTI 183
                                                                                                                                               67 HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRPNSG 126
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                                                            VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVBQLKPY
                                                                                      7 VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
                                                                                                                                                                                              EETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDND
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                                      Gaps
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         Length 550;
                                    1; Indels
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      Score 2798; DB 4;
Pred. No. 9.3e-249;
0; Mismatches 1;
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   97.6%;
Query Match
Best Local Similarity 98.7
Matches 543; Conservative
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2000US-024180P.
2000US-024617P.
2000US-024921P.

08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

29-SEP-2000; 2
29-SEP-2000; 2
20-CCT-2000; 2
02-CCT-2000; 2
02-CCT-2000; 2
02-CCT-2000; 2
02-CCT-2000; 2
03-CCT-2000; 2
03-CCT

Barash SC;

Ruben SM,

Rosen CA,

(HUMA-) HUMAN GENOME

17-NOV-2000; 2 10-DEC-2000; 2 05-DEC-2000; 2 05-DEC-2000; 2 06-DEC-2000; 2 06-DEC us-10-067-482-2.rag

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The invention relates to one of 238 disclosed human neoplastic disease—
associated polypeptides encoded by 171 disclosed cDNA sequences
(including their domains, epitopes, full-length proteins, allelic variants
or species homologues). Also included are there encoding nucleic acids, a
recombinant vector comprising the nucleic acid, a recombinant host cell
comprising the nucleic acid (expressing the protein), an isolated
antibody that binds specifically to the isolated polypeptide, preventing,
condition or a susceptibility to a pathological condition in a subject,
in a biological assay, and the gene corresponding to the CDNA sequence.
Condition or a susceptibility to an entibodies are useful for
the polypeptides, polynuclectides and antibodies are useful for
ameliorating medical conditions such as hyperproliferative diseases or
ameliorating medical conditions such as hyperproliferative diseases
concerned. autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
conficulating medical conditions such as hyperproliferative diseases
concerned. Lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
or haemolytic anaemia), haematopoletic or haematologic disorders (e.g.
canaemia or thrombocytopaenia), allergic reactions including asthma or
eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
                                                     New isolated human neoplastic disease-associated polypeptides and polymucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFFLGEVGNAAKWMLIVNWVQGSFWATIAEGLTLAQVTGQSQQTLLDILNQGQLASIFLD 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDND 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRPNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTBDHAWIKVBQLKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 DEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLFIQEGARLGRIPAEVVSTCDIIFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.6%; Score 2798; DB 7;
98.7%; Pred. No. 9.3e-249;
tive 0; Mismatches 1;
                                                                                                                                                 Claim 11; SEQ ID NO 417; 302pp; English.
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Best Local Similarity 98.7
Matches 543; Conservative
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WPI; 2003-786918/74.
                     N-PSDB; ADC46047
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The invention relates to human enzyme (ENZM) polypeptides and their corresponding polynucleotides. ENZM sequences are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional ENZM. The infectious disorders include immune disorders (anaemia, allergy or asthma), immune deficiencies (acquired immune deficiency syndrome; AIDS), immune deficiencies (addison's disease, diabetes or goitre), reproductive disorders (infertility or impotence), cardiovascular disorders (atherosclerosis or myocardial infarction), eye disorders and cell proliferative disorders (center).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP 120
                                                                                                                                                                        Human; enzyme; ENZM; immune disorder; infection; myocardial infarction; gene therapy; anaemia; acquired immune deficiency syndrome; infection; reproductive disorder: cardiovascular; eye; cell proliferation; cancer; AIDS; allergy; asthma; Addison's disease; diabetes; goitre; impotence; infertility; atherosclerosis; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human enzyme (ENZM) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chawla NK, Lee SY, Ring HZ, Lee EA, Forsythe IJ, Khare R;
Tran UK, Kable AE, Richardson TW, Emerling BM, Lindquist EA;
Baughn MR, Hafalia AJA, Jin P, Swarnakar A, Li JX, Marquis,
Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.6%; Score 2396.5; DB 6; Length 472; 85.2%; Pred. No. 8.1e-212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is human ENZM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 298-299; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overexpression of ENZM e.g. cancer.
                                   AAE38240 standard; protein; 472
                                                                                                                                      Human enzyme (ENZM) protein #32.
                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-2001; 2001US-0340357P.
20-DEC-2001; 2001US-0342962P.
21-DEC-2001; 2001US-0343558P.
22-JAN-2002; 2002US-0351107P.
                                                                                                                                                                                                                                                                                                                                                                         12-DEC-2002; 2002WO-US040161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE GENOMICS INC
                                                                                                    (first entry)
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Best Local Similarity
Matches 471; Conserv
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                                                                                                   20-NOV-2003
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                                                                   AAE38240;
RESULT 6
AAE38240
ID AAE3
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243 246 303 305 363 360 423 420

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2000US-0240960P.
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2000US-0241808P.
2000US-0241809F.
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2000US-0230437P.
2000US-0231243P.
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2000US-0231444P.
2000US-0231414P.
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2000US-0232081P.
2000US-0232081P.
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2000US-0232399P.
                                                      2000US-022954P.
2000US-022451BP.
2000US-0225213P.
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2000US-0225214P.
2000US-022526P.
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2000US-0237037P.
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2000US-0233065P.
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2000US-0234274P.
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2000US-0235484P
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20-OCT-2000; 2
20-OCT-2000; 2
20-OCT-2000; 2
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02-OCT-2000;
13-OCT-2000;
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20-OCT-2000;
20-OCT-2000;
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02-OCT-2000;
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        11-UUL-2000; 2
26-UUL-2000; 2
26-UUL-2000; 2
14-AUG-2000; 2
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14-SEP-2000;
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
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22-AUG-2000;
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01-SEP-2000;
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29-SEP-2000;
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27-SEP-2000;
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279
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                                                                                                                                                                                                                                                                                       480
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                                                                                                                                                                                                        360
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                NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD 180
                                              66
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                                                                                                                                                                                                                                                                                                                                                    EKCDLF1QEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM
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                                                 Q-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein, Seq ID No 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU20515 standard; protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0179065P.
2000US-0180628P.
2000US-018664P.
2000US-018974P.
2000US-0198174P.
2000US-0198123P.
2000US-0198123P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNDMSAVYRAYIH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; wound healing
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17-MAR-2000;
18-APR-2000;
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The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with the prevention, treatment and diagnosis of diseases associated with sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in
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Cagonists and antagonists) of the expression and activity of the secreted fagonists and antagonists of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies of any also be used as diagnostic agents for detecting the presence of (II) and samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The clisorders include for example: immune/autoimmune diseases (e.g. HIV) and multiple sclerosis), cancers and hyperproliferative disorders (e.g. and multiple sclerosis), cancers and hyperproliferative disorders (e.g. methanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease, neurological diseases (e.g. Alzhelimer's disease, parkinson's disease and charcot-Marie-Tooth disease), cardio-/
cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues.
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the production of antibodies and in assays to identify modulators
                                                                                                                                                                                                                                                                                                                                                                                49.0%; Score 1404; DB 4; Length 269; 99.3%; Pred. No. 1.3e-120; ive 0; Mismatches 2; Indels
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2000US-0184664P.
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2000US-0190076P.
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SCI INC HUMAN GENOME (HUMA-) SM Ruben Barash SC, Rosen CA,

WPI; 2001-465558/50. N-PSDB; AAS35012.

Novel polypeptides and polymucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.

Claim 11; SEQ ID NO 540; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and CDNA (AAS34767-AAS35050) and DNA

30-JUN-2000; 2000US-0215135P 07-JUL-2000; 2000US-0216647P 07-JUL-2000; 2000US-0216880P 11-JUL-2000; 2000US-0217487P 11-JUL-2000; 2000US-0217497P

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14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0224519P.
       disorders involving neoplastic disease such as hyperproliferation disorders involving neoplastic disease such as hyperproliferative disorders. July additive cancer, bladder cancer, brain stem Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders and renal disorders. Pulmonary disorders, reproductive disorders and renal in gene therapy. Advances sequences of the invention are also useful in gene therapy. Advances of the invention. Note: The sequence data disease associated polypeptides of the invention. Note: The sequence data obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences]
                                                                                                                                                                                                                                                                               ö
 sequences encoding for these polypeptides. The sequences of the invention
                                                                                                                                                                                                                                                                                                                                                       HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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                                                                                                                                                                                                                                                                                                                                                                                                             DEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTI 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoplastic disease—associated polypeptide; gene therapy; thyperproliferative disease; cancer; autoimmune disorder; diabetes; rheumatorid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haemotopietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury; inflammatory bowel disease; crohn's disease; neurodegenerative disorder; acute glomerulonophritis; end-stage renal disease; cance glomerulonophritis; end-stage renal disease; cardiovascular disorder; atherosclerosis; myocarditis; infectious disease; AIDS; canchexia; anorexia; wound healing; epithelial cell proliferation; Human.
                                                                                                                                                                                                                                                                                                4 VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVBQLKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VSLXLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neoplastic disease-associated gene 123 protein #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.3
Matches 267; Conservative
                                                                                                                                                                                                                  Sequence 269 AA;
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2000US-0231413P. 2000US-0231414P. 2000US-0232080P. 2000US-0232081P.

08-SEP-2000;

2000US-0231243P. 2000US-0231244P.

08-SEP-2000 08-SEP-2000

000US-0230438P

2000US-0229343P

01-SEP-2000;

23-AUG-2000 30-AUG-2000

01-SEP-2000; 05-SEP-2000; 05-SEP-2000 06-SEP-2000; 06-SEP-2000; 2000US-0232399P. 2000US-0232400P. 2000US-0232401P.

14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0233064P. 2000US-0233065P. 2000US-0234223P.

L-SEP-2000;

2000US-0234274P. 2000US-0234997P. 2000US-0235484P 2000US-0235834P

26-SEP-2000;

2000US-0236370P

29-SEP-2000;

2000US-0233063P.

14-SEP-2000;

2000US-0231968P. 2000US-0232397P. 2000US-0232398P.

New isolated human neoplastic disease-associated polypeptides and polymucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's

Claim 11; SEQ ID NO 540; 302pp; English

disease

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Barash SC;
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17-RXV-2000; 2000US-0249264P.
17-RXV-2000; 2000US-0249265P.
17-RXV-2000; 2000US-0249265P.
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17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-025031P.
05-DEC-2000; 2000US-0251331P.
05-DEC-2000; 2000US-0251338P.
06-DEC-2000; 2000US-025119P.
06-DEC-2000; 2000US-0251145P.
08-DEC-2000; 2000US-0251856P.
                                          02-CCT-2000; 2000US-0237040E.
13-CCT-2000; 2000US-023935F.
13-CCT-2000; 2000US-023935F.
20-CCT-2000; 2000US-0240960E.
20-CCT-2000; 2000US-024178FP.
20-CCT-2000; 2000US-024178FP.
20-CCT-2000; 2000US-024178FP.
20-CCT-2000; 2000US-024180FP.
20-CCT-2000; 2000US-024647FP.
08-NOV-2000; 2000US-024647FP.
08-NOV-2000; 2000US-024647FP.
08-NOV-2000; 2000US-024652FP.
08-NOV-2000; 2000US-024651P.
                               2000US-0237039P.
2000US-0237040P.
2000US-0239935P.
2000US-0239937P.
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2000US-0249216P.
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                                  02-OCT-2000;
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The invention relates to one of 238 disclosed human neoplastic disease-
associated polypeptides encoded by 171 disclosed CDNA sequences
c associated polypeptides encoded by 171 disclosed CDNA sequences
(including their domains, epitopes, full-length proteins, allella variants
cc fincluding their domains, ancluded are there encoding nucleic acids, a
crecombinant vector comprising the nucleic acid, a recombinant host cell
c recombinant vector comprising the nucleic acid, a recombinant host cell
c recombinant vector comprising the protein, an isolated
c cantibody that binds specifically to the isolated polypeptide, preventing,
c treating or a susceptibility to a pathological condition in a subject,
condition or a susceptibility to a pathological condition in a subject,
c in a biological assay, and the gene corresponding to the CDNA sequence.
c the polypeptides, polynucleotides and antibodies are useful for
c meliorating medical conditions such as hyperproliferative diseases or
c ameliorating medical conditions such as hyperproliferative diseases or
c ancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
c systemic lupus erythematosus, multiple scleroais, autoimmune thyroiditis
c or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
c anaemia or thrombocytopaenia), allergic reactions including asthma or
c czema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRPNSG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 DEKRKLSLSECKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 PESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQALTKKLKLCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VSLXLGGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.0%; Score 1404; DB 7; Length 269; 99.3%; Pred. No. 1.3e-120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human hepatoma-derived growth factor (HDGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-US006731.
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Best Local Similarity 99.3%;
Matches 267; Conservative
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WPI; 2003-786918/74. N-PSDB; ADC46170.

243

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Human hepatoma-derived growth factor-2 (HDGF-2) (AAW09404) shows 23% identity and 61% similarity over a 201-amino acid stretch to human HDGF, a mitogen for fibroblasts. Its amino acid sequence was deduced from a CDNA clone (AAT47520) isolated from a human umbilital wein endothelial tissue cDNA library. Recombinant HDGF-2 can be produced in transformed host (e.g. B. coli, Sf9, COS) cells. It is useful in stimulating tissue repair and tissue growth and can also be used to produce antibodies and
                                                                                                                                                                                  DNA encoding human-derived growth factor polypeptide - useful to promote wound healing as result of burns or ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                     screen for antagonists that retard tumour growth and reduce scarring
                                                                                                                                                                                                                                     Claim 7; Fig 2; 54pp; English
                                                        INC.
                  95WO-US006731
                                                     (HUMA-) HUMAN GENOME SCI
                                                                                         Rosen CA
                                                                                                                           WPI; 1997-043108/04.
N-PSDB; AAT47520.
                  05-JUN-1995;
                                                                                       Kunsch CA,
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45.0%; Score 1291; DB 2; Length 249; 99.6%; Pred. No. 3e-110; Live 1; Mismatches 0; Indels 243; Conservative Local Similarity Sequence 249 AA; Query Match Matches

120 120 180 240 9 9 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP 1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEGL KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD LTIPESSTVKGMMAGPWAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK 0; Gaps ICEE 244 241 İČED 244 61 61 121 121 181 241 ð g ð g δ g à g ð

ABU09982 standard; protein; 249 AA. 30-JUL-2003 ABU09982; RESULT 11 **ABU09982**

Human hepatoma-derived growth factor 2 (HDGF-2). (first entry)

Human; hepatoma-derived growth factor-2; HDGF-2; vasotropic; vulnerary; antinflammatory; gene therapy; vascular endothelial cell growth; re-vascularisation; ischaemic tissue; thrombosis; arteriosclerosis; cardiovascular condition; mesodermal induction; limb regeneration; owned healing; injury; burn; surgery; ulcer; neuronal growth; neuronal damage; neuronal discreer; neuronal growth; neuronal damage; neuronal discreer; neuronal growth; changer; ulcer; neuronal growth; hower regeneration; prindion; prindion; prindion; prindion; blancerte growth; bone regeneration; periodontal regeneration; tissue transplant; bone graft; skin aging; sunburn; keratinocyte growth; hair loss; hair-forming cell activation; melanocyte growth; haematopoietic cell growth; haematopoietic cell differentiation;

organ transplantation; mesodermal tissue; cell growth; bone marrow cell; organ transplantation; mesodermal tissue; cell proliferation; tumour; hypervascular disease; epithelial lens cell proliferation; extracapsular cataract restenosis; balloon angioplasty; inflammation; scar tissue. US2003022312-A1 Homo sapiens.

30-JAN-2003

15-NOV-2001; 2001US-00987755

95US-00464600. 99US-00263625. 05-JUN-1995; 05-MAR-1999;

(HUMA-) HUMAN GENOME SCI INC

Rosen CA; Kunsch CA,

WPI; 2003-447425/42. N-PSDB; ACA61586. Novel isolated human hepatoma-derived growth factor-2 polypeptide usefutor promoting healing in wounds, treating or prevention of Alzheimer's disease, stimulating chondrocyte growth, preventing skin aging, and preventing hair loss.

Claim 2; Fig 1; 21pp; English.

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disease conditions such as thromboate of the such actual due to various such as thromboate of disease conditions such as thromboate of cardiovascular conditions; stimulating mesodermal induction and limb cardiovascular conditions; stimulating mesodermal induction and limb conditions; burns, surgery, and ulcers; stimulating neuronal growth, and thus for treating or preventing neuronal damage occuring in certain centenconal disorders or neuronal disorders are useful for inhibiting the cell growth and therefore are useful for preventing abnormal cellular growth and proliferation e.g. in tumour formation or growth; preventing the cell stream of seases and preventing the proliferation of epithelial or neuron contains or growth there are useful for macrow. The antenders or neoplastic cells and proliferation e.g. in tumour formation or growth; preventing the cell are are neglial or preventing dispansed and preventing the proliferation of epithelial. lens cells after extracapsular cataract surgery; preventing restenosis after balloon angioplasty; and preventing inflammation and growth of scar tissue during wound healing. This is the amino acid sequence of human hepatoma-derived growth factor-2 (HDGF-2) The invention describes a polypeptide (I) having a deduced amino acid sequence of human hepatoma-derived growth factor-2 (HDGF-2) polypeptide sequence of 249 amino acids (82) as given in the specification, or its fragments, analogues or derivatives. (I) is useful for stimulating vascular endothelial cell growth, and thus is employed in treatment for stimulating re-vascularisation of ischaemic tissues due to various

Sequence 249 AA;

1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL Gaps ô Length 249; Indels 45.0%; Score 1291; DB 6; I oo 6%; Pred. No. 3e-110; Conservative Query Match Best Local Similarity Matches 243;

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120 KPYHAHKEEMIKINKGKRPQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRP 120 61 KPYHAHKEEMIKINKGKRPQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERGRP

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2000US-0236327P
2000US-02363687P
2000US-0236368P
2000US-0236370P
2000US-0236370P
2000US-0236370P
2000US-023703P
2000US-023703P
2000US-023703P
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2000US-0232081P.
2000US-0232397P.
2000US-0232399P.
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2000US-0241809P.
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2000US-0235836P.
2000US-0227182P
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
       23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
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08-NOV-2000;
08-NOV-2000;
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08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
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26-SEP-2000;
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02-0CT-2000;
02-0CT-2000;
03-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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20-OCT-2000;
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  180
                                                                                                                                                                                                                            Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer; multiple sclerosis; cancer; hyperproliferative disease; infection; daucher's disease; neurological disease; cerebrovascular disorder; thrombosis; wound healing.
            NSGDEKRKLSLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD
                                                                                                                                                                                                                Human secreted protein, Seg ID No 545
                                                                                                                                                        AAU20553 standard; protein; 260 AA
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2000US-0184664P-
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2000US-0190076P-
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2000US-0225447P.
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2000US-0216880P.
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14-AUG-2000;
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116-MAR-2000;
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28-JUN-2000;
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            243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 545; 753pp; English.
                                                2000US-0249212P.
200US-0249213P.
200UUS-0249214P.
200UUS-0249215P.
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2000US-0249265P
2000US-0249297P
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2000US-0250391P.
2000US-0251030P.
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Score 1291; DB 4; Length 260; Pred. No. 3.2e-110;

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Query Match Best Local Similarity

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                                                        61 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEBRSRP 120
                                                                     9
                                   MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL 71
                1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
                                                                                                                                                                                                                                                                                                                                        Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; mercular disorder; perroductive disorder; gastroincestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                                                                                                                                                                                                                                                      Novel human neoplastic disease associated polypeptide #180.
0; Indels
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2000US-0225268P.
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The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA disease associated polypeptides. The sequences of the invention sequences encoding for these polypeptides. The sequences of the invention compared in the disapposis. Ireatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative concer, childhood cerebellar astrocytoma, or concer, childhood cerebellar astrocytoma, or concer, childhood cerebellar astrocytoma, or concer, manual disorders, immune system cfor treating other disorders such as neural disorders, immune system cfor treating other disorders, reproductive disorders, manue system cisorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful consease associated polypeptides of the invention. Note: The sequence data contained in electronic format directly from WIPO at contained in electronic format directly from WIPO at corporation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides and polymuclectides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 474; 687pp; English
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Length 260;

Score 1291; DB 4; Pred. No. 3.2e-110;

45.0%;

Sequence 260 AA; Query Match Best Local Similarity

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14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-022547P.
14-AUG-2000; 2000US-022575P.
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12-AUG-2000; 2000US-022668P.
22-AUG-2000; 2000US-022668P.
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31-AUG-2000; 2000US-022688P.
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31-AUG-2000; 2000US-022989P.
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05-SEP-2000; 2000US-022950P.

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           KPYHAHKBEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP 120
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                                                                                                                                                                                                                                              LTIPESSTVKGMMAGPWAAFKWQPTASEPVKDADPHPHHFLLSQTEKPAVCYQAITXKLK 240
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                                                     Neoplastic disease-associated polypeptide; gene therapy; diabetes; rheumatoliferative disease; cancer; autoimmune disorder; diabetes; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; sthma; eczema; inflammatory disorder; ischemia-reperfusion injury; inflammatory bowel disease; crohn's disease; renal disorder; acte glomerulonephritis; end-stage renal disease; acte glomerulonephritis; end-stage renal disease; cardiovascular disorder; atherosclerosis; myocarditis; infectious disease; AIDS; canchai, anorexia; wound healing; epithelial cell proliferation; Human.
                                 1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
                                                                                                                                                                           NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD
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   1; Mismatches
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2000US-0180628P.
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17-MAR-2000; 2
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14-AUG-2000;
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The invention relates to one of 238 disclosed human neoplastic disease-associated polypeptides encoded by 171 disclosed cDNA sequences (including their domains, epitopes, full-length proteins, allelic variants or species homologues). Also included are there encoding nucleic acids, a recombinant vector comprising the nucleic acid (expressing the protein), an isolated antibody that binds specifically to the isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnoshing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the polypeptide, identifying an activity in a biological assay, and the gene corresponding to the CDNA sequence. The polypeptides, polymucleotides and antibodies are useful for detecting, preventing, diagnosing, prognosticating, treating or
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08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246525P.
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01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-02519P.
06-DEC-2000; 2000US-0251479P.
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08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
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                                                                                                                                                                                                                             KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP 120
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ameliorating medical conditions such as hyperproliferative diseases or cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple scalerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematologic disorders (e.g. anaemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
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                                                                                                                                                                                        KPYHAHKEEMIKINKGKRPQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                                                                                                   1 MAAVSLRIGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
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                                                                                                            Length 260;
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Best Local Similarity 99.6%; Pred. No. 3.2e-110;
Matches 243; Conservative 1; Mismatches 0;
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16-MAR-2000; 2000US-0189874P.
11-MAR-2000; 2000US-0189874P.
11-MAY-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0205515P.
20-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217487P.
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Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465558/50. N-PSDB; AAS34789 Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.

Claim 11; SEQ ID NO 317; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as superproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem Hodgkin's lymphomal. The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, pulmonary disorders, reproductive disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU21861 represent the novel human neoplastic

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disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM, Barash SC; WPI; 2003-786918/74.

New isolated human neoplastic disease-associated polypeptides and polynucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's N-PSDB; ADC45947.

Claim 11; SEQ ID NO 317; 302pp; English.

The invention relates to one of 238 disclosed human neoplastic disease-associated polypeptides encoded by 171 disclosed cDNA sequences (including their domains, epitopes, full-length proteins, allelic variants or species homologues). Also included are there encoding nucleic acids, a

New isolated nucleic acid detection reagent for detecting 1000 or more

Comprising the mucleic acid (expressing the protein), an isolated antibody that binds specifically to the isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding patrner to the polypeptide, identifying an activity in a biological assay, and the gene corresponding to the cDNA sequence. The polypeptides, polymucleotides and antibodies are useful for the polypeptides, polymucleotides and antibodies are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as hyperproliferative diseases or cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoletic or haematologic disorders (e.g. canemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury, ö 63 PYHAHKEEMIKINKGKREÇQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPN 122 181 241 242 2 AAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLK 61 recombinant vector comprising the nucleic acid, a recombinant host cell PYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPN 182 TIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKI SGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDL 0; Gaps Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. Length 250; 0; Indels Drosophila melanogaster polypeptide SEQ ID NO 9582. 44.9%; Score 1286; DB 7; 99.6%; Pred. No. 8.7e-110; iive l; Mismatches 0; Myers EW; ABB60930 standard; protein; 574 AA. Li PWD, 23-MAR-2001; 2001WO-US009231. 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. Local Similaricy hes 242; Conservative 26-MAR-2002 (first entry) Drosophila melanogaster Adams M, WPI; 2001-656860/75 (PEKE) PE CORP NY 242 CEE 244 243 ČED 245 N-PSDB; ABL05033. WO200171042-A2 27-SEP-2001 Venter JC, 62 122 Query Match ABB60930; Best Loca Matches RESULT 17 **ABB6093** 33333333333333333 g 8 g g à ò g à

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Tulip pistil
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                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of inscricides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3011), expressed DNA sequences (ABL16176-ABL3011), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 AEALALADRFSISLNDIIDIFDLTSMKSPMLLAKGKEWAKGDFNPQQPLSHMQRDLRLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                          234 RVETDALLASIAAKRAPNAIALLDRPVVTRPEAQVIDMSSRSNTLADRDIVPSEQTFGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                  19 YPPWPGKIVNPPKDL---KKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHA-HKEEMIKIN
                                                                                                                                                                                                                                                                                                                     KVKKNMGEGKKRVSSGSSERG-----SKSPL-----KRAQEQSPR----
                                                                                                                                                                                                                                                                                                                                                                                                       --HFHHFLLSQTEKPAVCYQAITKKLKICEEETGSTSIQAADSTAVNGSITPTDKKIGFL
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                              ----KRGRPPKDEKDLTIPESSTVKGMMAGPMAAFKWQPTAS-BPVKDADP----
                                                                                                                                                                                                               59;
                                  21pp + Sequence Listing; English
                                                                                                                                                                                            DB 4; Length
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 ALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
                                                                                                                                                                                            26.8%; Score 769.5; DB 4 32.6%; Pred. No. 1.5e-61; iive 108; Mismatches 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corn 3-hydroxyisobutyrate dehydrogenase #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE19927 standard; protein; 360
                                                                                                                                                                                                                 108;
                                     ID NO 9582;
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                                                                                                                                                                                                                   Conservative
     from Drosophila
                                                                                                                                                                                                        Similarity
                                                                                                                                                                          Sequence 574 AA;
                                      Disclosure; SEQ
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                 interactions
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The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HWG-CoA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polynucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from crin.pk0191.bl0, p0076.cwhan08r and p0118.chsbe01r clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEA 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                olated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, use produce transgenic plants having an altered expression of the enzyme.
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Branched chain amino acid degradation enzyme; HMG-CoA lyase;
3-bydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.1.31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 360;
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Pred. No. 1.6e-58;
7; Mismatches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                   Rafalski
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Les 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                      Hitz WD,
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                                                                                                                                                                 US6348339-B1
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123

445

183

505

us-10-067-482-2.rag

(first entry)

26-JUN-2003

AAE36392;

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Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway intermediates.
         Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide; enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase; gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant.
                                                                                                                                                                                                                                                                                      Claim 4; Page 110-111; 71pp; English.
                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                      Prabhu V,
                                                                                                             10-JUN-2002; 2002WO-US018230.
                                                                                                                                  08-JUN-2001; 2001US-0297198P
                                                                                                                                                                                    Flint D,
                                                                                                                                                                                                        2003-201331/19.
                                                                                                                                                                (PRAB/) PRABHU V.
                                                                                                                                                                                                                  N-PSDB; AAD55024
                                                                     WO2002101013-A2
                                                  Tulip pistil
                                                                                          19-DEC-2002
                                                                                                                                                                                    HG,
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The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrosynense and UDP-glucosyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal Tulipalin A sequences are used to immunise animals to produce polyclonal facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue

Sequence 290 AA;

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269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                  388
                                                                                                                                                                       448
                                                                                                                             181
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                                                                                                           ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                EVGFLGLGIMGKAMAVNLLRSGFRVTVWNRTLSKCNELLEGGASVGETPAAVIKKCKYTI
                                                                                                                                                               GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                                                                                                                                                 449 ATIAEGLTLAHVTGQSQQTLLDIINOGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                  Gaps
                                     .;
0
     25.1%; Score 720; DB 6; Length 290; 50.7%; Pred. No. 1.8e-57; ive 52; Mismatches 86; Indels
                                 86; Indels
                                                                                                                                                                                                                                                                      LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                       ||:||||
|Lalalgdenavsmpvaaaaneafkkarslglgdldfsavy 281
Query Match
Best Local Similarity 50.7°
Matches 142; Conservative
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AAE36392 standard; protein; 289 AA.

RESULT 20 AAE36392 ID AAE36

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The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrogenase and unb-glucoxyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylenesuccinate semialdehyde, alpha-methylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is mouse-ear cress (Arabidopsis thaliana) gamma-hydroxybutyrate dehydrogenase homologue
                                                                                                     Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide; enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase; gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant; mouse-ear cress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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                                                                             gamma-hydroxybutyrate dehydrogenase homologue.
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Pred. No. 3.7e-55;
.n. Wiematches 93; Indels
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                                                                                                                                                                                                                                                                                                                                                                           Ħ
                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 112-113; 71pp; English.
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                                                                                                                                                                                                                                                                                                                             DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                          Prabhu V,
                                                                                                                                                                                                                                                                 10-JUN-2002; 2002WO-US018230.
                                                                                                                                                                                                                                                                                            08-JUN-2001; 2001US-0297198P.
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                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                       Damude HG, Flint D,
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-201331/19
                                                                                                                                                                                                                                                                                                                           DU PONT DE PRABHU V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                   WO2002101013-A2
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242 LALALGDENAVSMPVAAAANEAFKKARSLGLGDLDFSAVIEA 283

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262 SITPTDKKIGFLGLGGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRIPAEVV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 AVTEPPARIGFLGLGIMGSPMAHNLLKAGVDLTVWNRTKSKCDPLISLGAKYKPSPEEVA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STODITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynuclectide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HMG-CoA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polymuclectides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polymucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is soybean 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from ses2w.pk0002.e5 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acid fragments encoding branched chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVQGSFNATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLEAPVSGNQQL,SNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKWMLIVN
                                                                                                                                             Branched chain amino acid degradation enzyme; HMG-CoA lyase; 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA; isovaleryl-CoA dehydrogenase; transgenic plant; soybean; EC 1.1.1.31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.8%; Score 682; DB 5; Length 345; 47.1%; Pred. No. 7.7e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JA;
                                                                                                                 Soybean 3-hydroxyisobutyrate dehydrogenase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Rafalski
                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO E I.
                           AAE19929 standard; protein; 345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 1; Col 33-36; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Kinney AJ,
                                                                                                                                                                                                                                                                                                                                     98US-0094990P.
                                                                                                                                                                                                                                                                                                      99US-00364230.
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Matches 136; Conservative
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Cahoon RE, Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                                            2002-204621/26.
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N-PSDB; AAD31750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 345 AA;
                                                                                                                                                                                                                                                                                                      29-JUL-1999;
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                                                                                          18-JUN-2002
                                                                                                                                                                                                                Glycine max.
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                                                            AAE19929
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The present sequence represents a plant gamma-hydroxy butyrate dehydrogenase (GHBDH). The specification also describes a plant gamma-minobutyric acid (GABA) transaminase (GABA-T). The proteins are involved in the metabolism of GABA in plants. GABA-T is used to transaminate GABA to form succinic semialdehyde, which may be converted to gamma hydroxybutyrate by GHBDH. The polynucleotides are used to produce GABA-T and GHBDH recombinantly. The proteins are useful for screening and isolation of homologous genes from other organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKGMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 ATIAEGLTLAHVTGQSQQTLLDILNQSQLASIFLDQKCQNILQGNFKPDFYLKYIQXDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel proteins related to gamma aminobutyric acid (GABA) metabolism, GABA-transaminase and gamma hydroxy butyrate dehydrogenase useful for screening and isolation of homologous genes from other organisms.
                                                                                                                                                                                                                                                                                                                    Misc-difference 1. .100
/note= "these residues are encoded by nucleotides 1-300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AMLSDPCAALSVVFDKGGVLEQICEGKGYIDMSTVDAETSLKINEAITGKGGRFVEGPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gamma-aminobutyric acid; GABA; GABA transaminase; GABA-T;
gamma-hydroxy butyrate dehydrogenase; GHBDH; succinic semialdehyde;
                                                                                                                                                                     Amino acid sequence of gamma-hydroxy butyrate dehydrogenase (GHBDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
286 HQQKDLRLALGLAESVSQPTPIASAANELYKVAKSNGLSDQDFSAVIEA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 679; DB 3; Length 289; 48.6%; Pred. No. 1.1e-53; Live 49; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Cauwenberghe OR;
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                 Ä.
                                                                                 AAB19491 standard; protein; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Fig 5; 48pp; English.
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Best Local Similarity 48.65
Matches 137; Conservative
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                            gamma hydroxybutyrate.
                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
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                                                                                                                AAB19491;
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99US-014252P.
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99US-0148319P.
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                    18-JUN-1999;
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      182 NAFSEGLVLADKSGLSSDTLXXIXDLGAMTNPMFKGKGPSMTKSSYPPAFPLKHQQKDMR 241
                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 8739.
                          509 LAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRA
                                                                      AAG10423 standard; protein; 353 AA
                                                                                                                                                                                                                                990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-0126564P.
990S-0126764P.
990S-0126785P.
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99US-0139119P.
99US-0139452P.
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                                                                                                     (first entry)
                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                  EP1033405-A2
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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23-APR-1999;
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28-APR-1999;
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01-JUN-1999;
03-JUN-1999;
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14-JUN-1999;
16-JUN-1999;
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29-MAR-1999
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06-APR-1999
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16-APR-1999
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08-JUN-1999
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478 ASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKAL 537
                                                                                           418 QAMGKISFFLGEVGNAAKWMLIVNWVQGSFWATIAEGLTLAHVTGQSQQTLLDILNQGQL 477
                                                                                                                                      272 NAPMYSLKGPSMIKSVYPTAFPLKHQQKDMRLALGLAESVSQSTPIAAAANELYKVAKSY 331
                                                           358 VDMSTVDADIVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCF 417
                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
RTAEKCDLF1QEGARLGRTPAEVVSTCD1TFACVSDPKAAKDLVLGPSGVLQGIRPGKCY
                                    Arabidopsis thaliana protein fragment SEQ ID NO: 8740.
                                                                                                                                                                                                                           AAG10424 standard; protein; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0126264P
990S-0126785P.
990S-0128234P.
990S-0128134P.
990S-0128414P.
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990S-0131449P.
990S-0132048P.
990S-0132407P.
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99US-0132486P.
99US-0132487P.
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            TTPSTRDELGTVS-
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23-APR-1999;
28-APR-1999;
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29-MAR-1999;
01-APR-1999;
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              21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.3%; Score 667.5; DB 3; 39.1%; Pred. No. 1.7e-52; ive 65; Mismatches 121;
                                                                                                                                                                                                                                                                        990S-0157865P

990S-0158029P

990S-0158239P

990S-0159239P

990S-0159239P

990S-0159239P

990S-0159231P

990S-0159331P

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990S-0160741P

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990S-0160768P

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990S-016089P

990S-0160980P
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9903-0161360P.
9903-0161361P.
9903-0161920P.
                                         99US-0149426P.
99US-014972P.
99US-0149929P.
99US-0149910P.
99US-0149910P.
99US-0151066P.
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99US-0152363P.
99US-0152363P.
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99US-0157117P.
99US-0157753P.
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99US-0155486P.
99US-0155659P.
99US-0156458P.
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99US-0162142P
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                                  99US-0149175P.
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Best Local Similarity 39.1%
Matches 146; Conservative
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28-OCT-1999;
29-OCT-1999;
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27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
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28-SEP-1999;
29-SEP-1999;
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14-OCT-1999;
14-OCT-1999;
                                          18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
25-AUG-1999;
         13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
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06-0CT-1999;
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14-OCT-1999
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99US-0134218P

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238 KLKICEBETGSTSIQAADSTAVNGSITFTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWN 297

9US-01347 9US-01319 9US-01319 9US-01353 9US-01356 9US-01367 9US-01375 9US-01375 9US-01375 9US-01375	UUS-01388 UUS-01394 UUS-01408	990S-0142154P. 990S-014236SP. 990S-0142363P. 990S-0142803P. 990S-0142874P. 990S-0143642P. 990S-014460SP. 990S-014408SP. 990S-0144333P. 990S-0144333P. 990S-0144333P. 990S-0144333P. 990S-0144333P. 990S-0144332P. 990S-0144332P. 990S-0144332P. 990S-0144332P. 990S-014532P. 990S-014532P. 990S-014532P. 990S-01450SP. 990S-01450SP. 990S-01450SP.
MAY - 199	100 100 100 100 100 100 100 100 100 100	01-70L-1999; 06-70L-1999; 08-70L-1999; 09-70L-1999; 13-70L-1999; 13-70L-1999; 15-70L-1999; 16-70L-1999; 16-70L-1999; 19-70L-1999; 19-70L-1999; 19-70L-1999; 19-70L-1999; 20-70L-1999; 21-70L-1999; 21-70L-1999; 22-70L-1999; 22-70L-1999; 23-70L-1999;
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990S-0144332P.
      9905-0132048P-
9905-013248P-
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9905-0139458P-
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990S-0144335P.
990S-0144352P.
990S-0144632P.
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99US-0142055P.
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99US-0142920P.
99US-0142977P.
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99US-0140991P.
99US-0141287P.
99US-0141842P.
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99US-0131449P
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20-JUL-1999;
20-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
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10-JUN-1999;
14-JUN-1999;
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17-JUN-1999;
18-JUN-1999;
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       30-APR-1999)
30-APR-1999)
04-MAX-1999)
06-MAX-1999)
06-MAY-1999)
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11-MAX-1999)
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 GNAAKMMIIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNIL 490
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                                                                                                              196 PMAAFKWOPTASEPVKDADPHFHHFLLSQTEKPAVC----YQALTKKLKICEBETGSTS 250
                                                                                                                                                 251 IQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEG 310
                                                                                                                                                                                   ARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTE 370
                                                                                                                                                                                                                         LAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEV 430
                                                                                                                                                                                                                                                                          215 GNGAAMKLVVMMIMGSMMASFAEGILLSQKVGLDPNVLVEVVSQGAINAPMYSLKGPSMI 274
                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                         QGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                                                                                                                                                                                           116; Indels 38; Gaps
                                                                         23.3%; Score 667; DB 3; Length 343; 39.4%; Pred. No. 1.9e-52; ive 64; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 8741.
                                                                                                                                                                                                                                                                                                                                                                   AAG10425 standard; protein; 285 AA
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99US-0123180P.
99US-0125788P.
99US-0126264P.
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99US-0161920P.
99US-0161932P.
99US-0161932P.
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                                                                                   Best Local Similarity 39.4%;
Matches 142; Conservative 6
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                                                                                                                                 PRIPLRFRPKPISP-
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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23-APR-1999;
23-APR-1999;
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   26-OCT-1999;
26-OCT-1999;
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29-OCT-1999;
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99US-014519EP.
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99US-0145218P.
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99US-0159637P.
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116-AUG-1999)
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20-AUG-1999)
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23-AUG-1999)
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04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
09-AUG-1999;
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03-AUG-1999;
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27-AUG-1999;
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30-AUG-1999;
31-AUG-1999;
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05-0CT-1999;
07-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
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14-OCT-1999;
14-OCT-1999;
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26-AUG-1999
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                                                                                                                                                                                                                                                                                                                              61 ESAIDVACGKNGAIFGISSGKGYVDVSTVDVASSILISKQIKDTGALFLEAPVSGSKKFPA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                     395 NDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLLVNMVQGSFMATIAEG
                                                                                                                                                                                                                                                                                                                                                                        455 LTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALG
                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Branched chain amino acid degradation enzyme; HMG-COA lyase; 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl COA; isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.1.31.
                                                                                                                                                                                                                           Query Match 21.9%; Score 629; DB 3; Length 285; Best Local Similarity 45.3%; Pred. No. 4.4e-49; Matches 125; Conservative 56; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                515 DAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corn 3-hydroxyisobutyrate dehydrogenase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Unknown
/note= "Encoded by NTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Unknown
/note= "Encoded by NCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE19926 standard; protein; 247 AA
 99US-0160741P-
99US-0160741P-
99US-016076P-
99US-0160710P-
99US-0160814P-
99US-0160818P-
99US-0160981P-
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99US-0161404P-
99US-0161404P-
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99US-0161920P-
99US-0161920P-
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18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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26-0CT-1999;
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990S-0139817P.
990S-0140353P.
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99US-0140823P.
99US-0140991P.
99US-0141287P.
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99US-0142803P.
99US-0142920P.
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99US-013244PP

99US-0132484P

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99US-0134218P-

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99US-0135621P-
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99US-0137528P.
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99US-0139452P.
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99US-0139492P.
                                         990S-0126264P.
990S-012678SP.
990S-0128234P.
990S-0128234P.
990S-0128077P.
990S-0130077P.
990S-0130674P.
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                              99US-0125788P
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29-JUN-1999;
30-JUN-1999;
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                                                     29-MAR-1999;
01-APR-1999;
06-APR-1999;
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                   09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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28-APR-1999;
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06-MAY-1999;
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23-APR-1999
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The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HWG-COA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polynucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from cen3n.pk0138.e1, ctaln.pk0052.d10 and p0037.crwak74r clones
                                                                                                                                                                                                                                                                                                                                                                                    284 SNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                 PSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                              AGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                  2 SNLIKAGCDVTVWNRTKSKCDPLLSLGAKYEPTPAQVASSCDVTFAMLADPQSAAEVACG
                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 SQQTILIDILNQGQLASIFILDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPNTLVEVISQGAISAPMFSLKGPSMVKAAYPPAFPLKHQQKDLS-SIGLADRV 234
                                                                                                                                                                                                                                                                                                                                        18.8%; Score 537.5; DB 5; Length 247; 45.3%; Pred. No. 9.8e-41; ive 47; Mismatches 80; Indels 1;
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                                                                                  Kinney AJ, Rafalski JA;
                                                                                                                                                                         Disclosure; Col 23-26; 40pp; English.
                                                            Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG41222 standard; protein; 168 AA
                                                           (DUPO ) DU PONT DE NEMOURS & CO
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                  99US-00364230.
                                       98US-0094990P
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Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana,
                                                                                   Cahoon RE, Hitz WD,
                                                                                                        WPI; 2002-204621/26.
                                                                                                                                                                                                                                                                                                                       Sequence 247 AA;
                                                                                                                      N-PSDB; AAD31747
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                  29-JUL-1999;
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31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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02-AUG-1999
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269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                                                                                              ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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0
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hes 76; Conservative
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06-0CT-1999;
08-0CT-1999;
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23-0CT-1999;
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Matches 76,
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05-MAY-1999;
06-MAY-1999;
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17-JUN-1999;
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23-JUN-1999;
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24-JUN-1999;
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11-MAY-1999;
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             \chi_{X} \otimes \chi_{X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 GRIPAEVVSTCDITFACVSDPKAAKDLVLGP-SGVLQGIRPGKCYVDMSTVDADIVTELA 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GQFAKTANQITIASTWLGLVEGLIXAHKAGLDVKKFLEAISTGAAGSKSIDLYGDRILKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 AAKYMLIVNWVQGSFWATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQG 492
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13.4%; Score 384; DB 3;
al Similarity 32.2%; Pred. No. 2.1e-26;
96; Conservative 48; Mismatches 152
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RESULT 30 AAG20954 ID AAG20954 standard; protein; 336 AA.

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Best Local Similarity 32.2³
Matches 96; Conservative 56 g δ g δ Б ò

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Search completed: September 16, 2004, 07:30:35 Job time : 69 secs

OM protein - protein search, using sw model

September 16, 2004, 07:28:53; Search time 19 Seconds (without alignments) 1502.587 Million cell updates/sec Run on:

US-10-067-482-2 2866

1 MAAVSLRLGDLVWGKLGRYP......AKALDQSDNDMSAVYRAYIH 553 Title: Perfect score: Sequence:

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Total number of hits satisfying chosen parameters: 389414 seqs, 51625971 residues Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database

Issued Patents AA:*

(Ggn2_6/ptodata/2/iaa/5A_COMB.pep:*
// Ggn2_6/ptodata/2/iaa/5B_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Semience 72 anni	4	à		6	7407					1792	٠,٧	247			6. Anr	o ur					1	· ~	· -	-		equence 8350
SUMMARIES	US-10-164-595-72	US-09-364-230-4	US-09-364-230-8	US-09-364-230-2	US-09-489-039A-9294	US-09-328-352-7407	US-09-252-991A-27650	US-09-107-532A-5109	US-09-489-039A-9424	US-09-252-991A-26001	US-09-252-991A-17923	US-09-711-164-438	US-09-252-991A-24727	US-09-328-352-4879	US-09-328-352-8139	US-09-364-230-6	US-09-134-000C-5460	US-09-364-230-12	US-09-489-039A-9860	US-09-489-039A-11448	US-09-252-991A-22003	US-08-760-745-5	US-08-760-745-3	US-08-760-745-1	US-09-364-230-10	US-09-788-657-22	US-09-489-039A-8350
DB	4	4	4	4	47	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	~	N	~	4	4	4
Length	547	360	345	247	307	299	543	299	304	324	330	292	295	303	326	342	247	350	309	309	221	237	240	235	234	1360	490
% Query Match	98.1	25.6	23.8	18.8	12.7	12.0	12.0	11.9	11.4	11.3	10.8	10.5	10.2	10.0	9.3	9.0	8.8	8.4	7.9	7.8	7.3		6.5	6.2	5.6	5.2	5.1
Score	2811	733	682	537.5	364	343.5	343	340	326	324.5	310	301.5	291	287.5	266	258.5	252	240.5	226.5	224.5	208	185.5	185.5	178.5	161.5	148.5	145
Result No.	1	7	٣	4	Ŋ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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99-543-6817 99-503-6917 90-509-802-9917 90-509-802-9918-902-9918-9918-9918-9918-9918-9918-9918-991	00000000000000000000000000000000000000	8-790-912-3 8-790-912-3 8-790-912-2 9-417-485D-6 9-417-485D-6 9-134-000C-380; 9-134-000C-502; 8-826-267-2 9-1016-000-2 8-515-251A-2 9-1016-000-2 8-515-251A-2 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726 9-976-594-726	9-377-155-7 9-69-974-7 9-69-974-7 9-392-714-22 9-50-236-1960 9-574-912-2 9-574-912-2 9-574-912-2 9-574-912-2 9-574-912-2 9-574-912-2 9-57-991A-274:7 9-69-974-17 9-66-974-17 9-66-974-17 9-66-974-17
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EK-----EGARLGRIPAEVVSTCDIIFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM 354
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                                                                                                                                                                                                                                                                                         Gaps
               Sequence 72, Application US/10164595
; Sequence 72, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Original rechnologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; CURRENT PELICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; SOFTWARES: PatentIn Version 3.1
; SEQ ID NO 72
; SEQ ID NO 72
                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                        Score 2811; DB 4; Length 547;
Pred. No. 3.6e-261;
0; Mismatches 1; Indels 6
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98.7%;
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                                                                                                                                                                                                                                                                                            Matches 546; Conservative
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                           Similarity
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US-10-164-595-72
RESULT 1
US-10-164-595-72
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Best Local
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Sequence 4, Application US/09364230 Patent No. 6348339 GENERAL INFORMATION:

RESULT 2 US-09-364-230-4

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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Rafalski, J. Antoni
APPLICANT: BL-178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
BARLIER APPLICATION NUMBER: 60/094,990
BARLIER APPLICATION NUMBER: 60/094,990
BARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOPTWARE: Microsoft Office 97
SEQ ID NO 8
APPLICANT: Hitz, William D.
APPLICANT: Hitz, Milliam D.
APPLICANT: Kinney, Anthony, Anthony D.
APPLICANT: Rafalski, J. Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o,
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184 PVSGSKKPAEDGQLVILAAGDKPLYDGMIPAFDVLGKKSFFLGEIGNGAKMKLVVNNMMG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 SFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQK 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 ITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 PVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88; Indels
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52.3%; Pred. No. 7.7e-62;
tive 47; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09364230; Patent No. 6348339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.6%.
Best Local Similarity 52.3%.
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Glycine max
US-09-364-230-8
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
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Sequence 7407, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PAPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/6/117,747
PRIOR PLILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLBAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 TMLPNSPHVQEVALGENGIIEGAKPGTVVIDMSSIAPLASREISEALKAKGIDMLDAPVS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 12.7%; Score 364; DB 4; Length 30
1 Similarity 28.7%; Pred. No. 1.7e-26;
81; Conservative 60; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 12.0%; Score 343.5; DB 4; Similarity 28.1%; Pred. No. 1.5e-24; 79; Conservative 56; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION WUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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US-09-328-352-7407
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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Matches 79; Conserv
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                                                                                                                                                                                                                                                                                                      LENGTH: 307
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kaney, Anthony J.
APPLICANT: Rafalskt, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
LENGTH: 247
                                           STCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTBLAQVIVSRGGR 381
                                                                                                                             382 FLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVN 441
                                                                                                                                                               442 MVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLK 501
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09364230 Patent No. 6348339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Acc. Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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US-09-364-230-2
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389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKAMLIVNMVQGSFM 448

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Sequence 9294, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:
ABTOLICANT: MAIC J. Rubenfield et al.
ABPELICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1999-02-18
FRIOR FILING DATE: 1999-02-18
FRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 GRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 LANPKEVAQEAEFIIVMVPDTPQVEDVLFRKDGIAEGVGPNKVVIDMSSISPTATKGFAE 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 KIKATGAQYLDAPVSGGEVGAKAATLSIMVGGCPNSFERALPLFQAMGKNITRVGGNGDG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 AKMMLIVNMVQGSFMATIABGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGN 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRAYIH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPVKDADPH------FHHFLLSQTEKPAVCYQAITKKLKICEEETGSTSIQAA 254
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                                               | | | : | | | | | | : | | | | | | EDPGFRISHQQVFSTCAAIGGSNWDHSALIKGLEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 RRNSSBERSRPNSGDEKR----KLSLSE---GKVKKNMGEGKKRVSS----GSSERGSK-
                    449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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                                                                                                                                251 TAVSYAKSLELNLPIAQKVSQLFENMLAAGDGELDHSGLIR 291
                                                                                                LAIALGDAVNHPTPMAAANEVYKRAKALDOSDNDMSAVYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GPHPGKPVGGDÓPRATRROPRPPRTGHRRDQLPL--
                                                                                                                                                                                                                         Sequence 27650, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-27650
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US-09-107-532A-5109
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US-09-252-991A-27650
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Best Local Simil
Matches 113; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 543
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 TMYGYPKDVEEIYYGQSGIFSADISGHINVDLTTSTPSLAEKTAKTAKEKGADALDAPVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 340; DB 4; I
Pred. No. 3.2e-24;
2; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCATION: (B) LOCATION 1...299 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5109: US-09-107-532A-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
PRELICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : : : | | :: | : : | 246 IALEEAEKMDLVLPATTQALKLYE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 LAIALGDAVNHPTPMAAAANEVYK 532
                                                                                                                                                                                                                                            ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
                                                                                                                                                  STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc feature (B) LOCATION 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 299 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.8<sup>§</sup>
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                          CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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RESULT

Sequence 5109, Application US/09107532A Patent No. 6583275

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PAPLICANT: Marc J: Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107136,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1723
                                   329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                                                                                                       220 QGLAEALHFARCAGLDGEAAMQVIGKGAAQSWQLENRHQSMLAGEFDFGFAVDWMRKDLS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 LAFAGLGLMGVPMCRRLLAAGYPLAVWNRSPGKRELLAAEGAKAVEVPARLAADAEILML 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 IVACNALVIABVVALAERAGVDASLVAPALAGGRADSKPLQILAPQMAESRYEPVKWHVR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 ATIAEGLTLAHVTGOSQQTLLDI-LNQGQLASIFLDQKCQNIL-----QGNFKP-DFYLK 501
                                                                                                                    389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                              100 CCVGNDDDLRAVALGEQGAFAGMAPGSLFVDHTTASAEVARELSLLAAERELGFLDAPVS
                                                                                                                                                  449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSR-GGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNNVQGSFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                               ::| ::| |::
280 ILLAEARRNGAQLPVTALVDQFYAEVQAMGGGRWDTSSL 318
                                                                                                                                                                                                                                                                                               509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score 310; DB 4; 28.6%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17923, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 438, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forsyth, R. Allyn
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-17923
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Patent No. 6521795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
RICH APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26001
                                                              GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 TDK-----KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 MMLIVNMVQGSFWATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFK 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 VSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 VSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.4%; Score 326; DB 4; Length 304;
29.9%; Pred. No. 7.4e-23;
tive 52; Mismatches 136; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGA-RLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 PDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 PQMQLAHALKDARLALSLAEP--HTMPGLENIAELWQQAADAGYAGEDLSAVYQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.3%; Score 324.5; DB 4; 26.5%; Pred. No. 1.1e-22; tive 62; Mismatches 142;
                                                                                                                                               FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9424
:-09-489-039A-9424
Sequence 9424, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 29.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 26.5
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                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-9424
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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Matches
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us-10-067-482-2.rai

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 326
                                                                                                                                                                                                                                                                                                                                       Sequence 4879, Application US/09328352

Sequence 4879, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. BRETON NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION UNMERR: US/09/328,352

CURRENT APPLICATION UNMERR: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GTIGAQAGTLTFMVGADEQTFNEVKPVLSHMGKNIVHCGDVGAGQIAKICNNLILGISMA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 TIAEGLTLAHVTGOSQQTLLDILN--QGQLASIFLDQKCQNILQG-----NFKPDFYLKY 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AVAEGWALGVKLGIDPQALAGVINTSSGRCWSSDVCNPWPHINENAPASRGYQDGFATQL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 IGFIGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
                                                                                                                          PVFGRTDVAEAGKLNIVVGGPEEAIEQVKALLEIMGQKTWFFGKDPRGAMAVKISGNFMI 180
                                                                                        445 GSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKP-DFYLKXI 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAFIGLGNMGGRMAQNLLKAGLKVYGYDLSEVAIQHFAEAGGIVCDSPQNAAKQADVVIT 69
386 PVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIV-NMVQ 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 303;
                                                                                                                                                                                           547
                                                                                                                                                                                                                   241 LKDVDLALSAGKRHNVPLPLASLLHDVLLEAIAHGDGESDWTAL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                           504 QKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.0%; Score 287.5; DB 4; 1 Similarity 25.5%; Pred. No. 3.7e-19; 74; Conservative 55; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-328-352-8139
                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-328-352-4879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 303
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            GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24727
LENGTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                         Η.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IMVPDTPQVEEVLFGENGCTKASLKGKTIVDMSSISPIETKRFARQVNELGGDYLDAPVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                    269 KIGFLGLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
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                                                                                                                                                                                                                                                                                                                                           DB 4; Length 292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                              10.5%; Score 301.5; DB 4; 27.7%; Pred. No. 1.6e-20; ive 51; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch
1 Similarity 28.9%; Pred. No. 1.6e-19;
82; Conservative 57; Mismatches 135
                   TITLE OF INVENTION: GENES ESSENTIAL FOR MI FILE REFERENCE: BLITRA.008A CURRENT APPLICATION NUMBER: US/09/711,164 CURRENT FILLING DATE: 2000-11-09 PRIOR APPLICATION NUMBER: US 60/164415 PRIOR FILING DATE: 1999-11-9 SUMBER OF SEQ ID NOS: 469 SOFTWARE: FASESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24727, Application US/09252991A
Patent No. 6551795
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                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                              78; Conservative
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Best Local Similarity
Matches 82; Conserv
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                                                                                                                                                                                                                                                                                                       US-09-711-164-438
                                                                                                                                                                                                            SEQ ID NO 438
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US-09-364-230-12

Sequence 12, Application US/09364230

Sequence 12, Application US/09364230

Sequence 12, Application US/09364230

Sequence 12, Application US/09364230

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Kinney, Anthoni

TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178

CURRENT APPLICATION NUMBER: US/09/364,230

CURRENT FILING DATE: 1999-07-29

EARLIER PILING DATE: July 31, 1998

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Microsoft Office 97
                                                                                                                                                                                        Sequence 5460, Application US/99134000C
| Patent No. 6617156
| Patent No. 6617156
| General Information: Sequence 5460, Application US/99134000C
| Patent No. 6617156
| APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: BNTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/99/134,000C
| CURRENT APPLICATION NUMBER: US 60/055,778
| PRIOR APPLICATION NUMBER: US 60/055,778
| PRIOR PILING DATE: 1997-08-15 | NUMBER OF SEQ ID NOS: 6812 | SEQ ID NOS: 6812 | SEQ ID NOS 5460 | SEQ ID NO 5460 | LENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 VSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 MMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFK 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AEVGAHALDAPVSGGDLGAKNGTLTIMVGGDQESYDTVLPIFKTFGKTFMLHGSAGKGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
8.8%; Score 252; DB 4; Length 24
Best Local Similarity 26.7%; Pred. No. 6.7e-16;
Matches 58; Conservative 41; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 PDFYLKYIQKDLRLAIALGDAVNHPTPMAAANEVYK 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 IYRKLCADGCELKDFSCAFR 333
530 VYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5460
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LOCATION: (154)
FEATURE:
NAME/KEY: UNSURE
                                                                                                                                                                   US-09-134-000C-5460
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LENGTH: 350
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APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REPERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
BARLIER APPLICATION NUMBER: 50/094,990
                                                                                                                270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGA------RLGRTPAEVVST 323
                                                                                                                                                                            47 IAFLGIGLMGSRMASRLIQAGFQVAVWNRTTSACEELIDIGAHALDLSNIGQYP---- 100
                                                                                                                                                                                                                                 324 CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL 383
                                                                                                                                                                                                                                                                        384 EAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMLLVNMV 443
                                                                                                                                                                                                                                                                                                                                                                                                    156 DSPVSGGTTGAEQGTLVVIFAGGDAQTIEALSPVYNVLSQRVTRWGDTGTGQATKICNQLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 VAANSALIAEAVALADRAGVDTTLLAPALAGG-----FADSKPPQILAPRNATHTFEFVQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 QGSFWATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNIL-----QGNFKP-D 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 STAVNGSITPTDKKIGFLGLGLAGSGIVSNLLKNGHTVTVWNRTAEKCDLFIQEGARLGR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 TPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKC----YVDMSTVDADTVTE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 LAQVI------VSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 ----QGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Gaps
                                                                          28;
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                    Length 326;
     9.3%; Score 266; DB 4; Length 32.
28.9%; Pred. No. 4.8e-17;
rative 42; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYLKYIQKDLRLAIALGDAVNHPTPMAAAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09364230 Patent No. 6348339 GENERAL INFORMATION:
  Query Match
Best Local Similarity 28.94
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 81; Conserv
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: NUCLEIC FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 TSIQAADSTAVNGSITPIDKKIGFLGLGLGLMGSGIVSNLLKMGHTVTVW--NRTAEKCDLF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 IQEGARLGRIPAEV--VSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVHKETSMAAHTNVC------VIGLGSMGMGAARACLQAG--LNTWGVDINPDNCRAL
                                                                    484 QKCQNILQGNFKPDFYLKYIQKDLRLALALGDAVNHPTPMAAAANBVYKRAKALDQSDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-11448
; Sequence 11448, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM; Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14342
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Best Local Similarity
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Sequence 9860, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 TGVPSSRNYDGGFISKLMAKDLDLAMASASGVGFKCPMGSBALBIYRKLCDBGCEFKDFS 337
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                                                                                                                                                                                                                                                                                                                                                                                               265 PTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 DITFACVSDPKAAKDLVLGPSGVL-QGIRPGK-CYVDMSTVDADTVTELAQ-----VLVS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                         38 PHMESVGFIGLGUNGSHMARNLVRAGYRVSVHDINBVAMKKFSDDGIPTKRSPLEVSESS 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QG-----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 GSAAKLCNNMAMAISMLGVSEAFALGONLGIKASTLTDIFNCSSARCWSSDTYNPVPGVM
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                                                                                                                                                                                                                                                   Length 350;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                       Query Match 8.4%; Score 240.5; DB 4; Best Local Similarity 26.1%; Pred. No. 1.5e-14; Matches 80; Conservative 41; Mismatches 166;
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                                                                                                              ; NAME/KEY: UNSURE
; LOCATION: (184)..(201)
US-09-364-230-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 CAFRHF 343
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US-09-489-039A-9860
                                             LOCATION: (176)
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67 KEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDEK 126
                                                                                                                                                                                                                                                                                                                                                         127 RKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKR----AQEQSPRKRGRPFK----D 177
                                                                                                                                                                                                        7 RIGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAH 66
                                                                                                                                               27;
                                                                                                               Length 237;
                                                                                                        6.5%; Score 185.5; DB 2; Length: 29.8%; Pred. No. 1.5e-09; trive 32; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            178 EKDLTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn E.
ITILE OF INVENTION: LUNG GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0169 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/760,745
FILING DATE: Herewith
GLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08760745
Patent No. 5972658
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
                                                                                                                                           65; Conservative
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                                                                                                        Query Match
Best Local Similarity
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               IMMEDIATE SOURCE:
                             ; LIBRARY: GenBa
; CLONE: 945419
US-08-760-745-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-760-745-3
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                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                        330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG 389
                                                                                                                                                                                                                                               270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
                                                                                                                                                                                                                                                                                                                                                         69 MLPAGQHVESLYLGDDGILARVAGKPLIDCSTIAPETARKVAEAAAAKGLTLLDAPVSG 128
                                                                                                                                                                                                                                                                                                                                                                                                390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNWVQGSFMA 449
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                      7.3%; Score 208; DB 4; Length 221; 27.5%; Pred. No. 9.5e-12; vative 36; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08760745
Patent No. 5972658
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
ITILE OF INVENTION: LUNG GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0169 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: FASTERN DOS
SUFTWARE: FASTESEQ Version 2.0
CURRENT APPLICATION DATA:
RILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
RPLICATION NUMBER:
FILING DATE:
ATTORNEY.
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 22003 LENGTH: 221
                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                  Query Match 7.3%
Best Local Similarity 27.5%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 TIAEGLTLAHVTG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 GTAEALALGVKNG 201
                                                                                                                                   US-09-252-991A-22003
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US-08-760-745-3

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APPLICANT: Calcon, Rebecca E.
APPLICANT: Calcon, Rebecca E.
APPLICANT: Altam D.
APPLICANT: Attack, Anthony J.
APPLICANT: Rafalsk, J. Antony J.
APPLICANTON: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: 199-172
CURRENT FILING DATE: 1999-07-29
EARLIER PLING DATE: J. 1999
EARLIER PLING DATE: J. 1998
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 VDMSTVDADTVTELAQVIVS-----RGGRF-----LEAPVSGNQQLSNDGMLVILAAGDR 407
                                                                              69 EMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDEKRK 128
                                                                                                                                                                129 LSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQ----EQSPR--KRGRPPKDEKDLT 182
                                                                                                                                                                                          408 GLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFWATIAEGLTLAHVTGQSQQT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 ILDILNQGQLASIFLD--QXCQNILQ-----GNFKPDFYLKYIQKDLRLAIALGDAVNHP 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 LINIFNCSSARCWSSDAYNPVPGLMEGVPSSGDYNGGFASKLMAKDLNLAVESAKLAGCK 193
                                                                                                                     67 KFGKPNKRKGFSEGLWEIEN-----NPTVKASGYQSSQKKSCVEEPEPEPEAAEGDGDKK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LDSSTIDPQTSRNLSATVINYILREKKGDWEKPFKLDAPVSGSVTAAEAGTLTFMVGGSE 73
                       GDL VWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVBQLKPYHAHKE
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Patent No. 6656736
GENERAL INFORMATION:
APPLICANT: Nacolaides, Nicholas
APPLICANT: Sass, Philip
APPLICANT: Kinzler, Kenneth
APPLICANT: Grasso, Luis
APPLICANT: Grasso, Luis
APPLICANT: Grasso, Luis
APPLICANT: Grasso, Luis
TITLE OF INVENTION: Methods for generating hypermutable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 161.5; DB 4;
23.2%; Pred. No. 3e-07;
tive 36; Mismatches 109;
                                                                                                                                                                                                                                                     183 IPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                                                                                                                                                 194 YPLTSQAQKIYTELCSVGHEAKDFSCAFRHY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 TPMAAAANEVYKRAKALDQSDNDMSAVYRAY
                                                                                                                                                                                                                                                                                                                                                                                US-09-364-230-10
; Sequence 10, Application US/09364230
Patent No. 6748339
; GENERAL INFORMATION:
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; ORGANISM: Glycine max

US-09-364-230-10
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Best Local Similarity
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US-09-788-657-22
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                                                                                                                                                                                                                                                             127 RKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQ----EQSPR--KRGRPPKDEKD 180
                                                                                                                                                                                                                    70 KEKFGKPNKRKGFSEGLWEIEN----NPTVKASGYOSSOKKSCVEEPEPEPEAAEGDGD 124
                                                                                           7 RLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAH 66
                                                                                                                                    69
                                                                                                                   Gaps
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6.2%; Score 178.5; DB 2; Length 235;
Best Local Similarity 29.6%; Pred. No. 7.1e-09;
Matches 63; Conservative 30; Mismatches 99; Indels 21
        Length 240;
          ; Score 185.5; DB 2; Length; Pred. No. 1.6e-09; 30; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                            180 ---KEAATLEVERPLPMEVEK-NSTPSEPGSGRGP 210
                                                                                                                                                                                                                                                                                                                                                181 LTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUNG GROWTH FACTOR VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08760745

Patent No. 5972658
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: MATRY, LUNG GROWTH FACTOR VARIF
ITLE OF INVENTION: LUNG GROWTH FACTOR VARIF
NUMBER OF SEQUENCES: 5
CORRESPONDENCES: 5
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0169 US
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SOFTWARE: FASTERO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,745
FILING DATE: Herewith
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 235 amino acids
               6.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                        64; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lungast01
               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 24
US-08-760-745-1
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
            NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA.
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 CSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFWATIAE-----GLTLAHVTGQSQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 QTFTE-WNEGELSSYLID----ITKDIFTKKDEDVKYL----VDVILDEAANKGTGKW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ETPRRILLMVKAGAĞTDSAİDSLKPYLDK------GDIİIDGĞNTFF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 QQIGVVGMAVMGRNLALNIESRGYTVSVFNRSREKTEEVIAENPGKKLVPYYTVQEFVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTLLDIINQGQLASIFLDQKCQNILQGNF-KPDFYLKYIQKDLRLAIALGDAVNHPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE--GARL--GRTPAEVVST
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                                                                                                                                                                                                                                                                                                                                                                                                      94; Gaps
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                                                                                                                                                                                                                                                                                                                                                      Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 486;
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     4.8%; Score 139; DB 4; Length 486
1 Similarity 19.2%; Pred. No. 0.00015;
64; Conservative 62; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                    5.1%; Score 145; DB 4; Length 490
22.0%; Pred. No. 3.9e-05;
ive 54; Mismatches 103; Indels
                         FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 EAPVSGNQQLSNDGMLVI---LAAGDRG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5380, Application US/09543681A; Patent NO. 6605709; GENEAL INFORMATION; APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- PMAAAANEVYKR 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 TSOSSLDLGEPLSLITESVFAR 309
                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                                                                                                    71; Conservative
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                    US-09-489-039A-8350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144
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                                                                                                                                                                                                                                                                                                                                                                                                                                         9 GDLVWGKLGRYPPWPGKIVNPPKD--LKKPRGKKC-FFVKFF-GTEDHAMIKVEQLKPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 GSKSK--EAOKGGHFYSAKPEILRAMORADEALNKDKIKRLELAVCDEPSEPEEEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --TSSHNSSDDKNRRNSSEERSRPNSGD-----EKRKLSLSBGKVKKNMGEGK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 GMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQ-----TEKPAVCYQAITKKLKI
                                                                                                                                                                                                                                                                                                                                                                                                 239;
                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1360;
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                                                                                                                                                                                                                                                                                                                                                                                            89; Mismatches 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 AHKEEMIKINKGKRFQQAVDAVEEFLRRAK---GKDQ
                                                                                                                                                                                                                                                                                                                                               5.2%; Score 148.5; DB 19.9%; Pred. No. 9.7e-05
FILLE OF INVENTION: yeast
FILE REFERENCE: 01107.00097
CURRENT APPLICATION NUMBER: US/09/788,657
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,336
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 SETKNTLRAFS-APONSE--
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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tes 140; Conserv
                                                                                                                                                                                                                           LENGTH: 1360
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260 NGSITPIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAE

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Sequence 8350, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:

US-09-489-039A-8350

RESULT 27

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APPLICANT: Gary Breton et.

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PatentIn version 3.0
  2000-06-02
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CURRENT FILING DATE:
                             NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin
SEQ ID NO 2
LENGTH: 786
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                             sb.
                                                                                                                                                                       , ORGANISM: Mus
US-09-509-802-2
                                                                                                                                                                                                                                                                                   Local Sim.
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105-052-91A-29147
1 Sequence 29147, Application US/09252991A
1 Sequence 29147, Application US/09252991A
2 Sequence 29147, Application US/09252991A
3 Fatent No. 6551795
3 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
5 SEQ ID NOS: 33142
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Retent No. 6489130

GENERAL INFORMATION:

APPLICANT: Immunex Corp.

APPLICANT: Wirea, G.D.

TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR)

FILE REFERENCE: 2889-US

CURRENT APPLICATION NUMBER: US/09/509,802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 RGLAMLDAPVSGGTAGAAAGTLTFMVGGDAEALEKARPLFEAMGRNIFHAGPDGAGQVAK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNOGQLASIFLD--QKCQNILQG--- 492
  ----EEFVDSLEKPRRILLMVKAGEA-TDKTIAALTPHLDKGDILIDGG 119
                                                                                                ILAAGDRGLYEDCSSCFQAMGK
                                                                                                                                                                          423 TS-----FFLGEVGNAAKMMLIVNMVQGSFMATIAEGLT-LAHVTGQSQQTLLDIL---
                                                                                                                                                                                                                                                                                      NQGQLASIFLDQKCQNIL----QGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                      528 NEVYKRAKALDQSDNDM-----SAVYRAYI 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GKWTSOSSLDLGVPVTLITESVFARYI 306
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                                                                380 GRFLEAPVSGNQQLSNDGMLV--
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US-09-252-991A-29147
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US-09-509-802-2
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                                                                                                                                                                                                                                                    ---TFQEITSETEDLCEKPDEEVKDLAHEPGEKSSLESKSE
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                                                                                                     11 LVWGKLGRYPPWPG-----KIVN-----PPKDLKKPRGKKCFFVKFFGTEDHAWI
                                                    Gaps
                                                    Indels 189;
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     Length
Score 135.5; DB 4;
Pred. No. 0.0007;
3; Mismatches 233;
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le : 23 secs
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                                                      83;
  4.7%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - p	OM protein - protein search, using sw model
Run on:	September 16, 2004, 07:29:27; Search time 718 Seconds (without alignments) 247.335 Million cell updates/sec
Title: US-10 Perfect score: 2866	US-10-067-482-2 2866

1 MAAVSLRLGDLVWGKLGRYP.....AKALDQSDNDMSAVYRAYIH 553 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

Total number of hits satisfying chosen parameters: 1342398 seqs, 321133274 residues Searched:

1342398

Post-processing: Minimum Match 100* Maximum Match 100* Listing first 100 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Published_Applications_AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1	Seguence 3, Applia	Sequence 4. Appli		Sequence 2. Appli	Sequence 474. App		505		Sequence 14. Appl	Sequence 16. Appl	Sequence 144794.		
SUMMARIES	US-10-067-482-2	US-10-103-313-417	US-10-067-482-4	US-10-103-313-540	US-09-987-755-2	US-10-103-313-474	US-10-103-313-317	US-10-425-114-50561	US-10-437-963-174476	US-10-167-547C-14	US-10-167-547C-16	US-10-424-599-144794	US-10-437-963-116017	US-10-425-114-42840
	41	14.	14	14	10	14	14	12	16	14	14	12	16	12
% Query Match Length DB	553	550	276	269	249	260	250	364	293	290	289	333	343	256
% Query Match	100.0	97.6	49.2	49.0	45.0	45.0	44.9	25.8	25.4	25.1	24.2	23.8	19.9	19.8
Score	2866	2798	1410	1404	1291	1291	1286	740.5	727	720	695	682	569	267
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equence 1744 equence 5208 quence 256, equence 4279 equence 5689	ce 9081, ce 15183 ce 57891 ce 11, A	equence 9563, equence 59047 equence 5655, equence 44990	equence 66289 equence 50872 equence 67475	equence 25587 equence 42674 equence 438, '	equence 60840, equence 74927, equence 61452, equence 146727	equence 24023 equence 25586 equence 73480 equence 224	quence 75520, quence 755, A quence 116817	equence 499 equence 300 equence 450	equence 476 equence 608 equence 569	equence 11, equence 16; equence 61;	Sequence Sequence Sequence	quence 41, equence 22(equence 132	ice 693 3e 511, 1ce 511	quence 1, Appli quence 3, Appli quence 3, Appli	equence /, # equence 14, equence 2, 7	equence 220, equence 2434	quence 1, Apequence 1640	equence 2486 quence 43, 7 equence 2266	equence 86, equence 51,	equence 308, equence 85,	sequence 20, Appl Sequence 346, App Sequence 346, App
10-437-963-174 10-282-122A-52 9-912-020-256 10-767-701-427 10-282-122A-56	10-156-761-908 -10-437-963-151 -10-282-122A-57 -10-123-965B-11 -10-282-122A-60	10-136-701-5303 -10-282-122A-5904 -10-282-122A-4499 -10-282-122A-4499	10-28	10-424-599-25587 10-282-122A-4267 10-287-274-438 10-425-114-53506	10-76 10-28 10-28	.10-424-599-24023 .10-424-599-25586 10-282-122A-7348 10-043-487-224	10-28 10-40 10-43	10-282-122A-4950 10-238-075-301 10-282-122A-4525	10-282-122A-4767 10-767-701-60846 10-335-977-5654	10-43 10-43 10-76	10-767-701-5238 10-282-122A-511 09-866-050A-651	9-768-826-41 09-833-245-2264 10-247-671-132	10-42 9-925 09-92	9-938	10-25 10-25	10-11	9-938 10-42	10-27 9-768 09-83	09-82	09-94	09-86 10-20 10-19
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481 FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS
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98.7%; Pred. No. 1.4e-230;
iive 0; Mismatches 1;
                                                                                                    Sequence 3, Application US/10067482;
Publication No. US20030148407A1;
FEBERAL INFORMATION:
APPLICANT: Origene Technologies, Inc.
TITLE OF INVENTION: Angiogenesis Dehydrogenase Gen;
FILE REFERENCE: 1U 102 R1.
CURRENT APPLICATION NUMBER: US/10/067,482
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
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US-10-103-313-417
; Sequence 417, Application US/10103313
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Best Local Similarity
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100.0%; Score 2866; DB 14; Length 553;
Best Local Similarity 100.0%; Pred. No. 3e-235;
Matches 553; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                          Sequence 2, Application US/10067482

Publication No. US20030148407A1

GENERAL INFORMATION:

APPLICANT: OriGene Technologies, Inc.

TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
FILE REFERENCE: 1U 102 R1

CURENT APPLICATION NUMBER: US/10/067,482

CURENT FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.1

FILE OF INVENTION OF 2.1
   US-10-201-858-346
US-10-205-890-346
US-10-208-024-346
US-10-174-581-346
US-10-176-483-346
US-10-176-913-346
US-10-176-915-346
US-10-176-915-346
US-10-106-815-308
US-10-005-815-308
US-10-013-907A-308
US-10-015-499A-308
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      -10-067-482-2
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                                                                                                                                                                                                                                                                                                                                                                                        1 MGSGIVSNLLKWGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAA
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                                                                                                                                                                                                                  Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 540, Application US/10103313
| Publication No. US20030082758A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PUZNOTOR:
| CURRENT APPLICATION NUMBER: US/10/103,313
| CURRENT FILING DATE: 2002-03-12
| NUMBER OF SEQ ID NOS: 653
| Prior Application removed - See File Wrapper or Palm | SOFTWARE: Patentin Ver. 2.0
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49.2%; Score 1410; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
Matches 276; Conservative 0; Mismatches 0;
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99.3%; Pred. No. 4.5e-111;
tive 0; Mismatches 2;
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Best Local Similarity 99.33
Matches 267; Conservative
          ; SEQ ID NO 4
; LENGTH: 276
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-482-4
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ORGANISM: Homo sapiens
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LOCATION: (4)
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US-10-103-313-540
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LENGTH: 269
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Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZO7C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030148407A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc.
TITLE OF INVENTION: Anglogenesis Dehydrogenase Gene FILE REFERENCE: 1U 102 R1
CURRENT APPLICATION NUMBER: US/10/067,482
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.6%; Score 2798; DB 14;
ilarity 98.7%; Pred. No. 1.9e-229;
Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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Best Local Similarity
Matches 543; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-103-313-417
                                                                                                                                                                                                                                                                                                                               SEQ ID NO 417
LENGTH: 550
TYPE: PRT
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US-10-067-482-4
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Best Local Similarity 99.6%;
Matches 242; Conservative 1
                                                             Conservative
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                                              Similarity
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US-10-425-114-50561
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US-10-103-313-474
                                              Best Local Sim:
Matches 243;
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LENGTH: 250
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                 181 PESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICE 240
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PESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICE 243
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US-10-103-313-474

US-10-103-313-474

Sequence 474, Application US/10103313

Publication No. US20030082758A1

FURBERCE INFORMATION:

APPLICANT: ROSSEN et al.

TITLE REFERENCE: PAZO7CI

CURRENT APPLICATION NUMBER: US/10/103,313

CURRENT APPLICATION NUMBER: US/10/103,313

NUMBER OF SEQ ID NOS: 653

NUMBER OF SEQ ID NOS: 653

NUMBER: Patentin Ver. 2.0

SEQ ID NO 474

LENGHA: 260

TYPE: PRT

CREANISM: Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 249;
                                                                                                                                                                   Sequence 2, Application US/09987755;
Publication No. US2030022312A1
GENERAL INFORMATION:
APPLICANT: Kunsch et al
TILLE OF INVENTION: Human Hepatoma-Derived Growth Factor-2
FILE REFERENCE: PF198D1C1
CURRENT APPLICATION NUMBER: US/09/987,755
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 09/263,625
PRIOR APPLICATION NUMBER: 09/464,600
PRIOR APPLICATION NUMBER: 08/464,600
PRIOR APPLICATION NUMBER: 08/464,600
PRIOR PILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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Pred. No. 1.7e-101;
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                                                                                 241 EETGSTSIQAADSTAVNGSITPTDKKIGF 269
                                                                244 EETGSTSIQAADSTAVNGSITPTDKKIGF 272
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Matches 243; Conservative
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; ORGANISM: human
US-09-987-755-2
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                                                                                                                       12 MAAVSLRIGEDLVWGKLGRYPPWPGKIVNPPXDLKKPRGKKCFFVKFFGTEDHAMIKVEQL
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                                                                                              1 MAAVSLRIGDLVWGYLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
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  Length 260;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
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                                                 Indels
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Score 1291; DB 14;
Pred. No. 1.8e-101;
1; Mismatches 0;
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Pred. No. 4.6e-101;
1; Mismatches 0;
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US-10-103-313-317
US-40-103-313-317, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
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388

61

181

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Sequence 14, Application US/10167547C
Publication No. US20030170653A1
Publication No. US20030170653A1
APPLICANT: L.1 du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
FURENT APPLICATION NUMBER: US/10/167,547C
CURRENT APPLICATION NUMBER: 60/297198
RIOR APPLICATION NUMBER: 60/297198
RIOR APPLICATION NUMBER: 00/297198
RIOR PILING DATE: 2003-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
                                                                                                                                                                                                                                                                                                         269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                      85; Indels
                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72412C.1.pep
US-10-437-963-174476
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                                                                                                                                                                                  Query Match
Best Local Similarity 52.19
Matches 146; Conservative
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                                         ORGANISM: Oryza sativa
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ORGANISM: tulip pistil
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Best Local Similarity
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US-10-167-547C-14
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LENGTH: 290
                                                                             FEATURE:
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Sequence 174476, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-05-14

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION AP476

LENGTH: 293
                                                                          APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen, Screen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 PKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQL 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: LIB3136-019-H11_FLI.pep
US-10-425-114-50561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 GDENAVAMPVSAAANBAFKKARSLGLGDQDFSAVY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 GDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
Sequence 50561, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
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US-10-437-963-174476
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APPLICANT: Wu, Wei
APPLICANT: Buckharror, Andrey A.
APPLICANT: Buckharror, Andrey A.
APPLICANT: Barbauk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
GURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEO ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 KIGFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                 STCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGR 381
                                                                                                                                                                                                               FLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAARMMLIVN 441
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                                                                                                                               34 AVTEPPARIGELGLGIMGSPMAHNLIKAGVDLIVWNRTKSKCDPLISLGAKXKPSPEEVA
                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      19.9%; Score 569; DB 16; Length 343; 39.8%; Pred. No. 1e-39; ive 51; Mismatches 83; Indels 5;
                             Length 333
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: PAT_MRT4530_19559C.1.pep
US-10-437-963-116017
                                                                       66
                               Score 682; DB 12;
Pred. No. 2.2e-49;
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                                                                       54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 116017, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                             23.8%;
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Matches 123; Conservative
                                                                           Conservative
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                                                       Similarity
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US-10-437-963-116017
US-10-424-599-144794
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LENGTH: 343
                                                                           Matches 136;
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                                     Query Match
Best Local
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                                                                                                                         Sequence 16, Application US/10167547C

Sequence 16, Application US/10167547C

Sequence 16, Application No. US2030170653A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: B.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: BLLYYO-lactone and its Intermediates

TITLE OF INVENTION: BLLYYO-lactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: 0010-17

FRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67

SOFTWARE: Microsoft Office 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(33.23.3)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 ATIAEGLTLAHVTGQSQQTLLDIINQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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       548
                             509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
24.2%; Score 695; DB 14;
Best Local Similarity 49.6%; Pred. No. 1.4e-50;
Matches 140; Conservative 49; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 144794, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-424-599-144794
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                                                                                                       RESULT 12
US-10-167-547C-16
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PELICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-0

PRIOR PELICATION NUMBER: 60/191,078

PRIOR PELICATION NUMBER: 60/206,846

PRIOR PELICATION NUMBER: 60/206,846

PRIOR PELICATION NUMBER: 60/200,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PELING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR PELING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Pamamoto, Robert
APPLICANT: Famamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Co. Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21 [33:313] B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 42440
LENGTH: 256
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                            267 FSLKGPSMVKAAYPTAFPLKHQQKDLRLALALAESVSQSIPTVAAANELYKVAXSLGLAD 326
482 LDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 VGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNI 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 LQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 GARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLOGIRPGKCYVDMSTVDADIVT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 ELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGE 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: 700580946_Fil.pep
US-10-425-114-42840
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Sequence 174477, Application US/10437963

Publication No. US200401233431

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                             US-10-425-114-42840
; Sequence 42840, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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Matches 111; Conservative
                                                                                                542 NDMSAVYRA 550
                                                                                                                                               327 ODFSAVIEA 335
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ORGANISM: Zea mays
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21/3221)B
CURRENT PAPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 144477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 LKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPSG 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 VLQGIRPGKCYVDMSTVDADIVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGD
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                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72413C.1.pep
US-10-437-963-174477
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.3%; Score 494.5; DB 16
52.3%; Pred. No. 9.9e-34;
tive 31; Mismatches 60;
                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(199)
FEATURE INFORMATION: unsure at all Xaa locations
FEATURE:
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180 TLFDVLDLGAIAN 192
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Best Local Similarity 52.3%
Matches 101; Conservative
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Gaps

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Indels

Mismatches 140;

57;

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Conservative
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Best Local Similarity
Matches 86; Conserv
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   83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KIGFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 TMYGYPSDVEEVYFNDNGILNNLKPQSYVVDMTTSKPSLAKKIYAAAKERNIFALDAPVS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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| Sequence 256, Application US/09912020
| Patent No. US20020045592A1
| GENERAL INFORMATION:
| APPLICANT: Zyskind, Judith
| APPLICANT: Trawick, John
| APPLICANT: Trawick, John
| APPLICANT: Forsyth, R. Allyn
| APPLICANT: Forsyth, R. Allyn
| APPLICANT: Forsith, R. Allyn
| APPLICANT: Forsith, R. Allyn
| APPLICANT: Tamancto, Robert T.
| APPLICANT: Yamancto, Jamancto,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: PatentIn version 3.1
SEQ ID NO 52083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 13.1%; Score 375; DB 12; Length 292; l Similarity 30.0%; Pred. No. 2.7e-23; 85; Conservative 55; Mismatches 143; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
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Pred. No. 1.4e-22;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Clostridium acetobutylicum
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29.4%;
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Best Local Similarity
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US-10-282-122A-52083
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ORGANISM: E.
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LENGTH: 299
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Best Local S
Matches 85
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Sequence 42795, Application US/10767701
Sequence 42795, Application US/10767701
Sequence 42795, Application US/10767701
Septimental INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Can, Yihua
APPLICANT: Can, Yihua
APPLICANT: Short Sequence and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535) B
CURRENT FAPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 TGSTSIQAADSTAVNGS---ITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 302
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                                                                                                                               GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                         ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                 187 AAMSEALTLATKAGVNPDLVYQAIRGGLAGSTVLDAKAPWVMDRNFKPGFRIDLHIKDLA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 KISFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGOSQQTLLDILNQGQLASIF 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 CDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAXDLVLGPS-GVLQGIRPGKCYVDMS
                                   269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                       329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                    LAIALGDAVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17849_1.pep
US-10-767-701-42795
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US-10-282-122A-56894
; Sequence 56894, Application US/10282122A
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FRIOR APPLICATION NUMBER: 60/20, 948
FRIOR FILING DATE: 2000-03-21,078
FRIOR PELING DATE: 2000-05-20
FRIOR APPLICATION NUMBER: 60/200, 727
FRIOR APPLICATION NUMBER: 60/200, 727
FRIOR PELING DATE: 2000-05-26
FRIOR PELING DATE: 2000-05-26
FRIOR PELING DATE: 2000-09-06
FRIOR PELING DATE: 2000-09-06
FRIOR PELING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-03
FRIOR FILING DATE: 2000-10-23
FRIOR PELICATION NUMBER: 60/253,625
FRIOR FILING DATE: 2000-12-2
FRIOR FILING DATE: 2001-12-2
FRIOR FILING DATE: 2001-12-2
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 2001-02-06
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FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-09
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION UNDER: US/10/282,122A
CURRENT FILING DATE: 2003-22
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IALDEAKKLDLPLPATQKATELYE 266
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ORGANISM: Enterococcus faecalis
                                                           . Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Carr, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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SEQ ID NO 56894
LENGTH: 296
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Wall, Daniel
Trawick, John
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Expo, Yihua
APPLICANT: Stou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brobazuk, Brad
APPLICANT: Brobazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRNCE: 38-21(5321)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 151834
LENGTH: 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 VQGSFWATIAEG--LTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKP-DFY 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.2%; Score 348.5; DB 14; Length 33.0%; Pred. No. 5.1e-21; Live 38; Mismatches 138; Indels
Sequence 9081, Application US/10156761
Fublication No. US2003011901841
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UUN
APPLICANT: HEDA, HARUO
APPLICANT: SHIKAWA, UUN
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SARAKI, YOSHIYIKI
APPLICANT: SARAKI, YOSHIYIKI
APPLICANT: SARAKI, YOSHIYIKI
APPLICANT: SARAKI, DANEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-39
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
FRIOR SEQIID NOS: 15109
SEQIID NO 9891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9081
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Best Local Similarity 33.0*
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US-10-123-965B-11
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LENGTH: 295
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                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                           127 GALAGLAPGGLLVDMTTSDPTLAAEIAEAAAKSCAAVDAPVSGGDRGARSATLSIFAGG 186
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                                                                                                                                                                                                       287 LKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPS-
                                                                                                                                                                                                                                                                   GVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAG
                                                                                                                                                           Gaps
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                                                                         Length 344;
                                                                                                           65; Mismatches 149; Indels
                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_51941C.1.pep
US-10-437-963-151834
                                                                         12.1%; Score 347; DB 16; 27.5%; Pred. No. 8.6e-21;
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                             84; Conservative
ORGANISM: Oryza sativa
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                                                                             Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Huang, Sheng-He TITLE OF INVENTION: E. Coli Virulence Determinants and Methods of Use Thereof FILE REFERENCE: USP1841A-SHH CURRENT APPLICATION NUMBER: US/10/123,965B CURRENT FILING DATE: 2002-12-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TW/GYPKDVEEIYYGQSGIFSADISGHILVDLTTSTPSLAEKIAKTAKEKGADALDAPVS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 ATIAEGLTLAHVTGQSQQTLLDIINQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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                                                                                                                                                                                                                                                                                                                                            Gaps
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or INUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 57891
LENGTH: 295
                                                                                                                                                                                                                                                                                            Length 295;
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28.7%; Pred. No. 7.9e-20;
iive 53; Mismatches 147; I
                                                                                                                                                                                                                                                                                         11.9%; Score 340; DB 12; 28.8%; Pred. No. 2.7e-20; ative 52; Mismatches 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAIALGDAVNHPTPMAAAANEVYK 532
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PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10123965B publication No. US20030099966A1 GENERAL INFORMATION:
                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
US-10-282-122A-57891
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
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148 MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL 507
                                                                                385 APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVG-----NAAKMMLI 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 VNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFY 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 AVNIQ-----ACAEAVVFLEKSGVDLKAALDVLGGGLAGSTVLTRKKDNFLHRDFKPGFR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                508 RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                  242 GIÁISEAKQMGLELPGLTLÁEKMÝQTLAEQGLSEEGTQALIKYY 285
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
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US-10-156-761-9563
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Matches 8
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62 ISWVGYPKDVEELYLGENGFLENLAVGTVAIDMTTSSPALAKKMAEFGREKGIGVLDAPV 121
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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.larity 27.1%; Pred. No. 1.5e-19;
Conservative 59; Mismatches 148; Indels (
                                                                                                                                                  243 LALENARLINTPLPNTATTQQLFSACAALGGKEWDHSALIRA 284
                                                                                                      LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                      Sequence 60763, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-33
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/230,347
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                -10-282-122A-60763
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US-10-282-122A-60763
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NUMBER OF SEQUENCES: 10031
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US-10-282-122A-44990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 285;
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32.7%; Pred. No. 1.8e-19;
iive 46; Mismatches 137;
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                              CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-03-66
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2001-12-22
PRIOR PELING DATE: 2001-12-22
PRIOR PELING DATE: 2001-12-22
PRIOR PELING DATE: 2001-12-29
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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ORGANISM: Helicobacter pylori
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 32.74
Matches 92; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
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269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KIGWIGLGAMGTPMATRLRDAGLEVSVYNRTESKAAPLKEKGVAVYTSPIDLAAKVDLVF
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                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
DOCATION: (B) LOCATION 1...285
SEQUENCE DESCRIPTION: SEQ ID NO: 5655:
US-10-335-977-5655
                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GTN-018 TELECOMMUNICATION INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44990, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
                                                                                                                                                ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 285 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617)742-4214
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SEQUENCE CHARACTERISTICS:
                                                                                                    STATE: Massachusetts
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 32...
These 92; Conservative
                                                                               CITY: Boston
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TITLE OF INVEN
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 200-2-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RIGFVGTGIMGMPMAMNLLKAGHQVKVWNRTSSKAVSLKEAGAYVCSELEQVGKDVEFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-3
PRIOR PILING DATE: 2000-05-3
PRIOR PELING DATE: 2000-05-26
PRIOR PAPPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-0-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-2
PRIOR PILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin version 3.1
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                                                                                                  Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 27.8%
Matches 78; Conservative
                                                                        Zyskind, Judith
                                                                                                                     Trawick, John
Carr, Grant
                                                                                               Wall, Daniel
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LENGTH: 290
                                                                                                                   APPLICANT:
APPLICANT:
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APPLICANT:
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US-10-282-122A-66301 ; Sequence 66301, Application US/10282122A ; Publication No. US20040029129A1 ; GENERAL INFORMATION:

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329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VAFLGLGTMGYPMAGHLOREGYDVCVYNRSSAKALRWVEEYAGRRADTPREACAGAELVF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGA-RLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - See File Wrapper or PALM
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26.5%; Pred. No. 5.4e-19;
tive 62; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THILE REFERENCE: ELITRA, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21,078

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

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US-10-282-122A-66301
Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                           Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
Matches 74; Conserva
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:

September 16, 2004, 07:28:53; Search time 19 Seconds (without alignments) 2799.680 Million cell updates/sec

US-10-067-482-2 2866 Title: Perfect score:

1 MAAVSLRLGDLVWGKLGRYP.....AKALDQSDNDMSAVYRAYIH 553 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	н	series	oxidoreductase [im				3-hydroxyisobutyra	probable dehydrode		2-hydroxy-3-oxopro	probable 3-hydroxy	3-hydroxyisobutyra	probable dehydroge	3-hvdroxvisobutvra	3-hvdroxvi sobut vra	3-hydroxyisobutyra	probable 3-hydroxy	3-hydroxyacid dehy	hypothetical prote	>				G	hypothetical prote	3-hvdroxvisobutvra	probable 3-hydroxy		T	
SUMMARIES		C70303	G90314	T08967	G97310	B69870	JQ0613	C91129	C85974	AE0897	S76381	AB3380	T34859	AC1558	B83979	AE1200	G71912	B81065	E81802	F83447	H82512	H83456	A98338	AI2944	G86901	T10635	C83232	B96015	G96013	D64782
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жo	Query Match	3.	13.7	13.4	•	•	•	2	12.8	12.6	11.8		٠	11.6	•	11.5			÷.	ä	11.1	•		•	•	11.0	٠		10.6	•
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A;Map position: 4
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hor
F;40-301/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T08967
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16519
A;Accession: T08967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G97310 dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC B. subtilis dehydrogenase related to 3-hydroxylicum c;Species: Clostridium acetobutylicum (;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 c;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001
                                                                                                                                                                               329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLBAPVS 388
                                                                                                                                                                                                                                                                                                        GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKOMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                              ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: ||| || || :::|||:
182 VSVVEGLILARSLGIDDDKLFSVLSTGAANSFTVQXYLPKIMKGDLNPGFKAAHLKKOLK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 GRIPAEVVSTCDITFACVSDPKAAKDLVLGP-SGVLQGIRPGKCYVDMSTVDADTVTELA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAKAMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQG 492
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                                                         269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                    24 ASSTISSDIITPSNTKIGWIGTGVMGRSMCGHLIKAGYTVTVFNRTISKAQTLIDMGANV 83
                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFDPGFYVNHFVKDLGICINECQRMGLALPGIALAQQLYLSLKAHGEGDLGTQALLLA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F19B15.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 18-Aug-2000
                                                                                                                     KVGFIGLGIMGFPMASNLLKAGYDLTVYNRTIEKAEKLGKMGAKVAHSPKEVAEVSEIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Cross-references: EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.150
A;Experimental source: cultivar Columbia; BAC clone F19B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 384; DB 2; Length 334;
; Pred. No. 4e-18;
48; Mismatches 152; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 YAMEIANSKSLPLLGTSLALQLYNAMVSLGIGELGTQGLVKVY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
      Mismatches 132;
         68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%;
32.2%;
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         Conservative
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Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: DNA
            83;
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: 690314
R;She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; ChanJong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Jong, I.; Jeffries, A.C.; Kozera, C.W.; Van der Oost, J.
A;Reference number: Asgan, A.D.; Sonsen, C.W.; Van der Oost, J.
A;Recerence number: A99139
A;Accession: G90314
A;Status: preliminary
A;Status: preliminary
A;Status: 1-289 <a href="https://documents.org/light-174">archiminary
A;Status: 1-289 <a href="https://documents.org/light-174">archiminary
A;Status: 1-289 <a href="https://documents.org/light-174">archiminary
A;Cross-references: GB:AEC06641; NID:g13814790; PIDN:AAK41774.1; GSPDB:GN00155
C;Genecics
A;Genecics
                                                                                                                                                                   3. Hydroxyisobutyrate dehydrogenase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Accession: C70303
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Residues: 1-288 AQF>
A;Residues: 1-288 AQF>
A;Residues: 1-288 AQF>
A;Cross-references: GB:AE000670; NID:92982779; PIDN:AAC06408.1; PID:92982783; GB:AE00065
C;Genetics:
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;3-265/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE-GARLGRTPAEVVSTCDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATIAEGLILAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 392.5; DB 2; Length 288; larity 31.7%; Pred. No. 9e-19; Conservative 61; Mismatches 132; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 289,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 392; DB 2;
Pred. No. 9.8e-19;
                      ALIGNMENTS
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29.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 90
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C; Accession: G97310

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A;Gene: yhaE
A;Map position: 68 min
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hon
C;Keywords: oxidoreductase
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A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-299 -KKOM>
A;Experimental source: strain Kl2, W3110
A;Experimental source: strain Kl2, W3110
A;Experimental source: strain Kl2, W3110
A;Experimental source: strain Kl2, Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                              268 KKIGFLGLGLMGSGIVSNILKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
                                                                                                                                                                                                                                                                                              328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli
NyAlternate names: hypothetical 31K protein (rnpB-sohA intergenic region)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession JQ6613, A65102
S;Komine, Y: Inckuchi, H.
submitted to JIPID, September 1990
A;Reference number: JQ0612
                                                                                                                                                                                                                                                                                                                                       183 MIGVAEAMAYAQKSGLEPENVLKSITTGAAGSWSLSNLAPRMLQGNFEPGFYVKHFIXDM
                                                                                                                                                                                                                            3 KTIGFIGLGVMGKSMASHILNDGHPVLVYTRTKEKAESILQKGAIWKDTVKDLSKEADVI
                                                                                                                                                                                                                                                                                                                                                                                                                              SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLJVNMVQGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 MATIAEGLTLAHVTGQSQQTLLDIINQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL
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A;Residues: 1-299 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;8-269/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAYI 552
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.8%; Score 367; DB 1; Length 299 clarity 29.4%; Pred. No. 4.7e-17; Conservative 57; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%; Score 368; DB 2; Le
26.7%; Pred. No. 3.8e-17;
:ive 65; Mismatches 144;
                                                                                             76; Conservative
                               Query Match
Best Local Similarity
Matches 76; Conserv
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Matches 83; Conserv
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C;Species: Bacillus subtilis
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Rivolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325, PMID:21359325
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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F;5-266/bomain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001437; PIDN:AAK81274.1; PID:g15026424; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.1%; Score 375; DB 2; Length 29 Similarity 30.0%; Pred. No. 1.3e-17; Si, Conservative 55; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                                      A; Residues: 1-292 <KUR>
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A, Status: preliminary
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Best Local Simil
Matches 85; C
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coli (strain K-12)

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A,Gene: yhaE
C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Ticle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MuID:21534947; PMID:11677608
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc
C;Keywords: oxidoreductase
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C;Genetics:
                                                                                                                                                                                                                                               389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMALIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                             449 ATIAEGUTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                            187 AAMSEALTLATKAGVNPDLVYQAIRGGLAGSTVLDAKAPMVMDRNFKPGFRIDLHIKDLA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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                                                                                                                                      329 ACVSDPKAAKDLVIGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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                                                       Length 299;
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1 Similarity 28.7%; Pred. No. 1.1e-16;
80; Conservative 58; Mismatches 141; Indels
                                                    Similarity 29.4%; Score 367; DB 2; Length 29
Similarity 29.4%; Pred. No. 4.7e-17;
33; Conservative 57; Mismatches 140; Indels
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A,Molecule type: DNA
A,Residues: 1-294 <PAR>
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                                                              Query Match
Best Local
C;Genetics
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                                      449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 12.8%; Score 367; DB 2; Length 299; Il Similarity 29.4%; Pred. No. 4.7e-17; 83; Conservative 57; Mismatches 140; Indels
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                                                                                                     247 NALDTSHGVGAQLPLTAAVMEMMQALRADGLGTADHSALACY
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hor
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: AL035478; PIDN: CAB3613.1; GSPDB: GN0070; SCOEDB: SC2G5.26c
                                                                                                                                                                                                                                                                                                                                                     BAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNA--AKM---ML 438
                                                                                                                                                                                                                                                                324 CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL 383
                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                                                                    62 ADFVFACIGNDDDLRSVTVGADGAFSTWKKDAIFIDNTTASAEVARELDKEAQKRGFHFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable dehydrogenase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
C;Accession: T34859
                                                                                                                                                                        266 TDKKIGFLGLGLMGSGIVSNL-LKMGHTVTVWNRTAEKCDLFIQE-GARLGRTPAEVVST
                                                                                                                                                                                                                                                                                                                                                                                                                                             439 IVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDF
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                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 OKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
                                                                                     Length 291;
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11.7%; Score 334; DB 2; Length 296;
Best Local Similarity 28.6%; Pred. No. 7.1e-15;
Matches 82; Conservative 53; Mismatches 142; Indels 1
                                                                                                                                  Indels
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                                                                              11.7%; Score 335; DB 2; Le
27.3%; Pred. No. 6e-15;
:ive 65; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                           Conservative
                                                                         Query Match
Best Local Similarity
Matches 79; Conserv
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
C;Keywords: oxidoreductase
F;6-267/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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                                                                                                                                                       probable 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) - Synechocystis sp. (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLG----RTPAEVVSTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 DITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 DIILTCVGDEKDVQQLILGSGGIAEYAKPQALIIDCSTIGKTAAYELATNLKLQGLRFLD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQ 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                          C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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Local Similarity 29.6%; Pred. No. 3.8e-15;
es 85; Conservative 50; Mismatches 144; Indels
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  LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                      A, Reference number: S74322; MUID: 97061201; PMID: 8905231
                            C,Species: Synechocystis sp. A;Variety: PCC 6803
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-291 «KUR»
A; Cross-references: GB: AE
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A, Status: preliminary
A, Molecule type: DNA
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C;Genetics:
A;Gene: BMEI1024
A;Map position: I
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Best Local S:
Matches 85
509
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3-hydroxyisobutyrate dehydrogenase (B. subtilis YkwC protein) homolog lmo1005 [imported]
3-hydroxyisobutyrate dehydrogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: ABI200
C;Accession: ABI200
C;Accession: ABI200
C;Accession: ABI200
C;Accession: ABI200
C;Accession: ABI200
C;Accession: ABI201
C;Buthard, B.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.,
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matachors: Kreft, J.; Sindes, M.; Ticheria, Paguez-Boland, J.A.; Voss, H.; Wehland, A;Hitle: Comparative genomics of Listeria species
A;Reference number: ABI077; MUID:21537279; PMID:11679669
A;Accession: ABI200
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
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A;Molecule type: DNA
A;Residues: 1-286 <GLAS
A;Cross-references: GB:NC_003210; PIDN:CAC99083.1; PID:g16410407; GSPDB:GN00177
A;Experimental source: strain EGD-e
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                                                                                                                                                                  328 PACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTBLAQVIVSRGGRFLBAPV 387
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EKIGEVGTGVMGSSMAGHILEAGYEVLVYTRTKTKAEDLLDKGALMVETPGELANKVDIL 61
268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
                                                   probable 3-hydroxyacid dehydrogenase - Helicobacter pylori (strain J99)
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11.5%; Score 331; DB 2; Length 286;
Best Local Similarity 27.1%; Pred. No. 1.1e-14;
Matches 77; Conservative 59; Mismatches 148; Indels
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3-hydroxyisobutyrate dehydrogenase BH2634 [imported] - Bacillus halodurans (strain C-125 S-pecies: Bacillus halodurans (species: C.)Dac-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 (spacession: B83979
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Retus: preliminary
A;Molecule type: DNA
A;Retus: preliminary
A;Molecule type: DNA
A;Reterences: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06353.1; GSPDB:GN0C
A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06353.1; GSPDB:GN0C
A;Cross-references: GB:AP001516; A;Gene: BH2634
C;Genetics:
A;Gene: BH2634
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc
                                                                                         3-hydroxyisobutyrate dehydrogenase (B. subtilis YkwC protein) homolog lin1004 [imported]
C; Species: Listeria innocus
C; Species: Listeria innocus
C; Decies: Listeria innocus
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AC1558
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Dominquez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Accession: AC1558
A;Status: preliminary
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1558
A;Status: preliminary
A;Residues: 1-286 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96235.1; PID:g16413463; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: lin1004
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hd
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Matches 75; Conserv
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hypothetical protein NWA1773 [imported] - Neisseria meningitidis (strain 22491 serogroup CySpecies: Neisseria meningitidis (5.5pecies: Nay-2000 #sequence_revision 05-May-2000 #text_change 09-Nov-2001 CyAccession: E81802 Ryparkhill. J.; Acthman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell Filoroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Arithe: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A;Reference number: A81775; MuID:20222556; PMID:10761919
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F;9-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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A;Residues: 1-289 <PAR>
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85001.1; PID:g7380415
A;Experimental source: serogroup A, strain Z2491
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                                                                                                                                                                                                                                                                                                269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                     329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTBLAQVIVSRGGRFLBAPVS 388
                                                                                                                                                                       68 LMVSDYAAVCDIL---NGVRDGL-AGKIIVNMSTISPTENLAVKALVEAAGGQFAEAPVS 123
                                                                                                                                                                                                                                                       389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                          449 ATIAEGLTLAHVIGOSQOTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                            389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable 3-hydroxyisobutyrate dehydrogenase PA1576 [imported] - Pseudomonas
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 LMVSDYAAVCDIL---NGVRDGL-AGKIIVNMSTISPTENLAVKALVEAAGGQPAEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 QIGWIGLGOMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELVRDYPVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 LAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||: | : | : | : | 244 LAVXELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
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Best Local Similarity 30.04
Matches 84; Conservative
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A;Gene: NMA1773
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C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 1-2-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 1-2-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: G71912
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1199
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71912
A;Accession: G71912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <ARN>
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CiSpecies: Neisseria meningitidis
CiSpecies: Neisseria meningitidis
CiSpecies: Neisseria meningitidis
CiSpecies: Neisseria meningitidis
CiAccession: B81065
Firettelin, H: Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; H. din, H: Vamathevan, J: Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. A; Huthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
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                                                                                                                                                                                                                                                                                                                                                                                         GB:AE001439; NID:94155127; PIDN:AAD06158.1; PID:9415512
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;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: jhp0585
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;3-260/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .Gene: NMB1584
.Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
:9-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KIGWIGLGAMGTPMATRLRDAGLEVSVYNRTESKAAPLKEKGVAVYTSPIDLAAKVDLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TMLSD-KAAIDAVLAPKFWEQMSK--KIVVNMSTIAPLESLSLEKIAQKHQATYLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%; Score 330; DB 2; Length 285; 32.7%; Pred. No. 1.2e-14; Live 46; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: strain J99 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: AE001491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 32.78
Matches 92; Conservative
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A;Molecule type: DNA
A;Residues: 1-289 <TET>
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C;Accession: H83456
R;Stover, C.K.; Pham. X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brn adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathos
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 csTO-
A;Cross-references: GB:AE004579; GB:AE004091; NID:g9947455; PIDN:AAG04889.1; GSPDB:GN001:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: PA1500
C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable oxidoreductase PA1500 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                 206 INGLSEGLMLAEQAGLDIPNLVACLKNGAAGSWOMENRALTMSQEKFDFGFAIDWMIKDL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGGEVGAKAATLSIMVGGCPNTFERALPLFQAMGKNITRVGGNGDGQTAKVANQIIVALN 181
                                                86 LTCVGNDDDVRSMTTAATGAIPAMKPGAVLIDHTTTSALLABELSAAAQQAGLHFMDAPV 145
                                                                                                             SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KIGFLGLGLMGSGIVSNLLKMGHTVTV-WNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 FACVSDPKAAKOLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV
                                                                                                                                                                                                                                448 MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL
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11.1%; Score 318; DB 2; L.
Best Local Similarity 29.0%; Pred. No. 8.2e-14;
Matches 83; Conservative 51; Mismatches 150;
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: HB2512
R;Heidelberg, J.R.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R;Heidelberg, J.R.; Eisen, J.A.; Vanter, J.C.; Fraser, C.M.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82512
A;Status: pre-liminary
A;Moolecule type: DNA
A;Residues: 1-315 <HBI>A;Cross-references: GB:AE004344; GB:AE003853; NID:99657378; PIDN:AAF95921.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
A;Genetics:
A;Amp position: 2
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
                                 Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: PR3447
A;Accession: PR3447
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: LNA
A;Residues: 1-288 <STO>
A;Experimental source: strain PA01
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llarity 26.9%; Pred. No. 8.3e-14;
Conservative 52; Mismatches 154;
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Matches 76; Conserv
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A;Cross-references: EMBL:AL080282; GSPDB:GN00062; ATSP:T13X14.90
A;Experimental source: cultivar Columbia; BAC clone T13K14
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Residues: 1-371 <BEV>
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A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A,Reference number: A97359; MUID:2160851; PMID:11743194
A,Accession: A98338
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-315 <XUX>
A;Residues: 1-315 <XUX>
C;Genetics:
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C'species: Agrobacterium tumefaciens
C'species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C'Accession: AI2944
R'Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
R'Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A;Map position: linear chromosome
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                               268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
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A.Experimental source: strain C58 (Dupont)
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11.1%; Score 318; DB 2; Length 31
Best Local Similarity 27.0%; Pred. No. 9e-14;
Matches 75; Conservative 58; Mismatches 139; Indels
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Matches 75; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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hypothetical protein ywjF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
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A;Experimental source: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 RLAIALGDAVNHPTPMAAAANEVYKR----AKALDQS 540
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Best Local Similarity 27.99,
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conserved hypothetical protein SMb20668 [imported] - Sinorhizobium meliloti (strain 102 C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Aug-2001 #text_change 30-Sep-2001 C;Accession: G56013 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna R;Finan, T.M.; Weidner, S.;
449 ATIAEGLTLAHVTGQSQQTLLDI-LNQGQLASIFLDQKCQNIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74; Conservative
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Matches 74; Conserv
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                           A;Map position: 4
A;Introns: 38/3; 68/2; 106/3; 157/1; 208/3; 240/3; 288/2; 316/3; 343/2
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;40-344/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448
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                                                                                                                                                                                                                                                                                                                                                                  451 IAEGLTLAHVTGQSQQTLLDILN--QGQLASIFLDQKCQNILQG-----NFKPDFYLKYI 503
                                                                                                                                                                                                                                                                                                                                                                                        257 TSEALAIGQSLGISASTLTEVLNTSSGRCWSSDAYNPVPGVMKGVPSSRDYNGGFASKLM 316
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                                                                                                                                                                                                 308 QEGARIGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQG---IRPGKCYVDMSTVD
                                                                                                                                            248 STSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI
                                                                                                                                                            Gaps
                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 310; DB 2; Length 296; 28.6%; Pred. No. 2.8e-13; ive 57; Mismatches 136; Indels
                                                                                        Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                          OKDLRLAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRAY
                                                                                       ; Score 316; DB 2; Length 37;
; Pred. No. 1.5e-13;
58; Mismatches 154; Indels
                                                                                             11.0%;
25.3%;
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Best Local Similarity
Matches 83; Conserv
                                                                                                           Similarity
              A, Gene: ATSP:T13K14.90
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Best Local S:
Matches 88
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probable 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) [imported] - Sinorhizobium me C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 #yaritle: The complete sequence of the 1,683-Kb pSymb megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
Science 293, 668-672, 2001
Apathors: Kahn, D.; Kahnan, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A,Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A,Reference number: A96039; MUID:21360234; PMID:11474104
A,Contents: annotation
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: glxR, SMb20679
A,Genome: plasmid
C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
C,Keywords: oxidoreductase
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                                                                      502 YIQKDIRLAIALGDAVNHPTPWAAANEVYKRAKALDQSDNDMSAVYRAY
                                                                                                                 AIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
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61 IMVPDIPQVEEVLFGENGCTKASLKGKTIVDMSSISPIETKRFARQVNELGGDYLDAPVS 120

GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448

550

LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA

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Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cyspecies: B96736
Rytheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Arature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                        449 ATIAEGLTLAHVTGOSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                          181 EAVSEALLFASKAĞADPVRVRQALMGGFASSRILEVHGERMIKRTFNPGFKIALHQKDLN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005173; NID:g6714326; PIDN:AAF26019.1; GSPDB:GN00141
                                                                                          329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                            241 LALQSAKALALNLPNTATCOELFNTCAANGGSQLDHSALVQA 282
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A,Molecule type: DNA
A,Residues: 1-297 <STO>
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General SWb20668
A; Genome: plasmid
C; Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
                                                                                                                 C;Species: Escherichia coli common control of the color of the complete genome sequence revision 17-Sep-1997 #text_change 01-Mar-2002 C;Accession: D64782 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C;Accession: D64782 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc Science 277, 1453-1462, 1997 *Science 277, 1453-1462, 1997 *A;Title: The complete genome sequence of Escherichia coli K-12.
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9834, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing
A;Reference number: A95842; MUID:21396508; PMID:11481431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFL-GEVGNAAKMMLIVNMVQGSF 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAKAAKGELTIMASGSPQAFAAARPALDAMAAKVYELGGTAGTGAAFKMINQILAGVH 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KIAVIGLGSMGFGMACSMKSAGLDVLGYDVAPPAVERFVAEGGRGAGTPGEAVTGADIIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.6%; Score 303.5; DB 2; Best Local Similarity 26.4%; Pred. No. 7.7e-13; Matches 75; Conservative 56; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-hydroxyisobutyrate dehydrogenase homolog b0509
                                                                          A;Accession: G96013
A;Status: preliminary
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C.Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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28.3%; Pred. No. 1e-12,
...ve 56; Mismatches 130;
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A;Cross-references: GB:AE000157; GB:U00096; NID:g1786716; PIDN:AAC73611.1; PID:g1786719;
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc
F;3-263/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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shown

A; Accession: D64782 A; Status: preliminary; nucleic acid sequence not shown; translation not

A; Molecule type: DNA

A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503

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Search completed: September 16, 2004, 07:31:11

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Indels

51; Mismatches 152;

Length 292;

10.5%; Score 301.5; DB 2; llarity 27.7%; Pred. No. 1e-12; Conservative 51; Mismatches 152;

Local Similarity les 78; Conserv

Best Loca Matches

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       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                    REDLINE=98044043; Pubmed=9344377;

RA KURDE F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA KURS F., Ogasawara N., Moszer I., Botchin A., Borchert S.,

RA Acevedo V., Bertero M.G., Beseives P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

R. Broullet S. Bruseli C.V., Caldwell B., Capuano V., Carter N.M.,

RA Borizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Harkoof C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Haga K., Harwoof C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Haga K., Harwoof C.R., Mones L.,

RA Guiseppi G., Guy B.J., Haga K., Harwoof C.R., Mones L.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobaysshi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Mediaw A., Laridnois S., Lauber J., Lazarevic V.,

RA Mediaw A., Laridnois S., Lauber J., Lazarevic V.,

RA Mediaw N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Moore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sato T., Scanlan E., Serleich S., Schroeter R., Scoffone F.,

RA Tosato V., Uchiyama S., Vandenbol M., Vansarotti A.,

RA Takeuchi M., Tamakoshi A., Taraka T., Tarpstra P., Tognoni A.,

Voshida K., Yoshikawa H.F., Zumatein E., Yoshikawa H., Danchin A.,

RA Tosato V., Wabuutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Winters P., Wapat A., Zamamoto G. the Gram-positive bacterium Bacillus R.,

RH Heller Companyer E., Roche E., Yoshikawa H., Danchin A.,

RH Heller Companyer E., Roche E., Yoshikawa H., Danchin A.,

RH Heller C., Waller E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E.,
                                                                                                                                                                                                                                                             to cse-15.";
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-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                             "Sequence of the Bacillus subtilis chromosome from ykuA submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                      10-0CT-2003 (Rel. 36, Last sequence update)
Hypothetical oxidoreductase ykwC (EC 1.1.-.)
YKWC OR BSU13960.
                   288 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEL; 299111; CAB13269.1; -.
PTR; B69870; B69870; Subtilist; BG13328; YkwC.
InterPro; IPR002204; 3hydroxisobut_dh
InterPro; IPR006183; GFGD.
InterPro; IPR006118; GFGD.NAD.
Ffam; PR03446; NAD binding 2; I.
PRINTS; PR00076; FFGDHDRGNĀSE.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                  STRAIN=168;
Scanlan E., Devine K.M.;
                       STANDARD;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                         Bacillus subtilis.
                                                                                                                                                                             NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                          MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL 507
                                                                                                                                                                                                                          62
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MEDLINE-20388234; PubMed=12471157;
MEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T. Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komine Y., Inokuchi H.; "Precise mapping of the rnpB gene encoding the RNA component of RNase P in Escherichia coli K-12.";
                                                                                                                                                                            268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT
                                                                                                                                                                                                         328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
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28-FEB-2003 (Rel. 41, Last annotation update)
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate
Hypothetical protein; Oxidoreductase; NAD; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAYI 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 GIALEEABLMGEEMPGLSLAKSLYDKLAAQGBENSGTQSIYKLWV 287
                                                                                 ; Score 368; DB 1; Length 28; Pred. No. 3.2e-16; 65; Mismatches 144; Indels
                                        976DD9098DB47A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AA
                       BY SIMILARITY
                                                                                           12.8%; Score 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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GARR OR B3125 OR C3880.
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30-MAY-2000 (Rel. 39, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                        288 AA; 30711 MW;
                                                                                                                   26.78;
                                                                                                                                        76; Conservative
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                                                                                             Query Match
Best Local Similarity
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                          ACT SITE
SEQUENCE
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P23523
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                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 ATIABGLTLAHVTGQSQQTLLDIINQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                    Monterrubio R., Baldoma L., Obradors N., Aguilar J., Badia J., "A common regulator for the operons encoding the enzymes involved in B-galactarate, D-glucarate, and D-glycerate utilization in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                   Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.; "Evolution of enzymatic activities in the enolase superfamily: characterization of the (D)-glucarate/galactarate catabolic pathway
                                                                                                                                                                                 J. Bacteriol. 183:2672-2674 (2000).
-!- CATALYTIC ACTIVITY: (R.-glycerate + NAD(P)(+) = 2-hydroxy-3-
oxopropanoate + NAD(P)H.
-!- PATHWAY: D-galactarate metabolism; third step.
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.8%; Score 367; DB 1; Length 29 29.4%; Pred. No. 3.8e-16; ive 57; Mismatches 140; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17DA392C2253278C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRRAMS; TIGR01505; tartro sem red; 1.
PROSITE; PS00895; 3 HYDROXXISOBUT DH; 1.
Oxidoreductase; NAD; Complete profeome.
ACT SITE 170 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, D90212; BAA14238.1; ALT_INIT.
EMBL, U1897; AAA7728.1; ALT_INIT.
EMBL, AAC00394; AAC76159.1; ALT_INIT.
EMBL, AE016767; AAN82321.1; ALT_INIT.
                                                                                                                          MEDLINE=20225875; PubMed=10762278;
                                                                         in Escherichia coli.",
Biochemistry 37:14369-14375 (1998).
                          MEDLINE=98447507; PubMed=9772162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 AA; 30427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Conservative
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RESULT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mk region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
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PIK; 576381.
InterPro; IPR002104; 3hydroxisobut_dh.
InterPro; IPR006118; 6PGD.
InterPro; IPR006118; 6PGD.
InterPro; IPR006115; 6PGD MAD.
Pfam; PF03446; NAD. binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
PROSTITE; PS00895; 3 HYDROXYISOBUT DH; 1.
HYPOCHELICAI protein; Oxidoreduciase; NAD; Complete proteome.
ACT_SITE 175 HYPOSTITE; PS0111411TY.
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                                                                                                                                                                                                                                                   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                       is-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase SIr0229 (EC 1.1.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 AA
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Q9SUGO; Q8LC25;
16-OCT-2001 (Rel. 40, Created)
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STANDARD;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                  Synechocystis sp.
                                                                                                                                                                                                                                                                              NCBI_TaxID=1148;
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RA MEJULES-2008-348 PLONGG-10-17198;

RA MEJULES-2008-348 PLONGG-10-10-17198;

RA PODIT T. DUSCETCHOEFT A., STICHERMA W., ENTIAN K.-D., TETYN N., HARLIS B., MASORGE W., BARLIS B., MASORGE W., MASORGE W., BOOLTY M., SCHMIGHTEN T., RECKEET B., POSTECEL T., AND STATE B., AND STATE B., AND STATE B., AND STATE B., AND STATE B., AND STATE B., AND STATE B., AND STATE B., AND STATE B., DOTECEL T., ZIMMERTAND W., Wedler H., Radley P., LANDSHAM S.-A., MCCUIJABN B., BILDAM L., ROODEN J., AND STATE B., DOTECEL T., SCHMIGHTS B., AND STATE B., AND STATE B., DOTECT T., DOTECE T., SCHMIGHTS B., AND STATE B., DOTECT T., DOTECE T., DOTECE S., VAND STATE B., DOTECT T., BRAM S.-A., MCCUIJABN B., BILDAM T., AND STATE B., DOTECT T., BRAM S.-A., MCCUIJABN B., BABTISHOR T., AND STATE B., DOTECT T., BRAM S., MANDSTATE S., VAND STATE B., DOTECT T., BRAM SOLIDAR B., DOTECT T., DOTECT T., DOTECT T., DOTECT T., TOTAL B., AND STATE B., DOTECT T., DOTECT T., SCHARL B., LANDSTATE B., DOTECT T., SCHARL B., LANDSTATE B., AND STATE B., DOTECT T., SCHARL B., L., DOGGET T., SCHARL B., L., DOGGET T., SCHARL B., MULLIBRAT B., RAYABLAR S., AND STATE B., DOTECT T., SCHARL B., MINGLAY W., LONDOURT S., MONDOURT S., MANDOURT S., MASTER C., POLING M., PEDDER T., SCHARL B., SCHMIGHT M., ENDER T., SCHARL B., SCHMIGHT M., ENDER T., SCHARL B., SCHMIGHT M., LOCKER S., GE HAAN M., MARTS A., MONDOURT S., TAGON D., 1968SE T., SCHARL B., SCHMIGHT W., LOCKER S., BENGER T., MONDOURT S., TAGON D., 1968SE T., SCHARL S., SCHMIGHT W., LOCKER S., PERROS S., GE HAAN M., MARTS C., SCHARCE M., AND SCHARL S., SCHARL S., SCHMIGHT W., LOCKER S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S., SCHARL S.,
             10-OCT-2003 (Rel. 42, Last annotation update)
Probable 3-hydroxylsobutyrate dehydrogenase, mitochondrial precursor
                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Surantophyta; Magnoliophyta; Erassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Troukhan M., Alexandrov N., Lu Y.-P., Flavell
10-OCT-2003 (Rel. 42, Last sequence update)
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402:769-777(1999).
                                                                               AT4G20930 OR T13K14.90
                                                             (EC 1.1.1.31) (HIBADH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                        eurosids II; Bra:
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brover V., Tro
Feldmann K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana
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-!- CAUTION: Ref.1 sequences differ from that shown due to erroneous

gene model prediction.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 QEGARIGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQG---IRPGKCYVDMSTVD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 ADTVTELAQVIVSRGGR------FLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 -QGQLASIFLDQKCQNILQG----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 SSGRCWSSDAYNPVPGVMKGVPSSRDYNGGFASKLMAKDLNLAAASAEEVGHKSPLISKA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSLHRFSSSSQNSN---QFQNVGFIGLGNMGFRMVNNLIRAGYKVTVHDINRDVMKMFT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=E97426617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobactería; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-HYDROXYISOBUTYRATE
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002204; 3hydroxisobut dh.
PROSITE; P800895; 3 HYDROXYISOBUT DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Mitochondrion;
Transit peptide.
TRANSIT 1 34 MITOCHONDRION (BY SIMILARITY)
CHAIN
35 347 PROBABLE 3-HYDROXYISOBUTYRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEHYDROGENASE.
NAD (ADP PART) (POTENTIAL)
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6ED2E87CC3DE191C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 328; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 35, Last sequence update) (Rel. 42, Last annotation update)
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S -> F (IN RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEVYKRAKALDOSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                    EMBL, ALO80282; CAB45888.1; ALT SEQ.
EMBL, AL161554; CAB79093.1; ALT_SEQ.
EMBL, AY086845; AAM63893.1; -.
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347 AA; 37364 MW;
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219
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10-OCT-2003
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CONFLICT
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241 LALQSAKALALNLPNTATCQELFNTCAANGGSQLDHSALVQA 282

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGEIGAREĠTĽSÍMVGĠĎEAVFÉRVKPĽFEĽĽĠKNITĽVGGNĠĎGQTCKVANQIIVALNI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KLGFIGLGIMGTPMAINLARAGHQLHV-TTIGPVADELLSLGAVSVETARQVTEASDIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                           Cusa E., Obradors N., Baldoma E., Badia J., Aguilar J.,
"Genetic analysis of a chromosomal region containing genes required
for assimilation of allantoin nitrogen and linked glyoxylate
metabolism in Escherichia coli.",
J. Bacteriol. 181:7479-7484 (1999).
-!- CATALXTIC ACTIVITY: (R)-glycerate + NAD (P) (+) = 2-hydroxy-3-
oxopropanoate + NAD (P)H.
                                                                                                                 Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- INDUCTION: By glyoxylate.
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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R EcoGene; EG12465; glar.

R InterPro; IPR002204; 3hydroxisobut_dh.

R InterPro; IPR006115; 6FGD_NAD.

DR InterPro; IPR006398; Tartro_sem_red.

DR InterPro; IPR006398; Tartro_sem_red.

DR PRINTS; PR00076; 6FGDHDRGNASE.

DR TIGRFAMS; TIGR01565; Lartro_sem_red; 1.

PROSTITE; PS00895; 3 HYDROXYISOBUT_DH; 1.

KW Oxidoreductase; NAD; Complete profeome.

ACT SITE 169 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%; Score 301.5; DB 1; Length 292; 27.7%; Pred. No. 4.8e-12; Live 51; Mismatches 152; Indels 1;
                                         sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Glyoxylate catabolism.
-!- INDUCTION: By glyoxylate.
                                                                                                                                                                                                                                                      MEDLINE=20069628; PubMed=10601204;
                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000157; AAC73611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U89279; AAB93851.1; -.
                                       "The complete genome sequen
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 27.7%
Matches 78; Conservative
                                                                                                                                                                                                                                    STRAIN=K12 / ECL1;
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.
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MEDINE=2338825'; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Sheamen C.W., Schuler G.D.,
A Lecchul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diacchenko L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,
A Diacchenko L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,
A Diacchenko L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M.J. Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                AND STANDER CONTROLL OF TASSURE OLFACTORY ORGAN;

RAY MEDLINE=22354683; PubMed=12466851;

RAY AGAZAKI Y. FURUNO M., RASUKAWA T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Baldarelli R., Fletcher C.F., Forrest A., Frazer K.S.,

RA Baldarelli R., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanajott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescole G.,

RA Perrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Senghe C.A., Setou M., Shimada K.,

RA Sandelin A., Schneider C., Senghe C.A., Setou M., Shimada K.,

RA Wilming D.G., Wynshaw-Boris A., Vanagisawa M., Yang I., Yang I.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa T.,

RA Birney E., Havashizaki Y.,

RA Birney E., Havashizaki Y.,

RA Birney E., Rogers J.,

RA Birney E., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                               10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                       335 AA.
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Nature 420:563-573(2002).
                                                       STANDARD;
                                                                                                                                                                                                         1.1.31) (HIBADH).
                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                          Q99L13; Q8BJY2;
                                                     DH3I MOUSE
                                                                                                                                                                                                                              HIBADH.
RESULT 6
DH3I_MOUSE
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Eukaryota; Metazoa;
                                                                              SECUENCE FROM N.A.
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208
68
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 IQEGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDAD 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 LGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILN--QGQLASIFLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 KCQNILQG-----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 TVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 GSLAAVCSRSMA---SKTP----VGPIGLGNMGNPMAKNLMKHGYPLILYDVFPDVCKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
                                                                                  SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-HYDROXYISOBUTYRATE DEHYDROGENASE.
    CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor HEBADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NAD; Mitochondrion; Transit peptide.
TRANSIT 1 35 MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Mismatches 157; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A -> S (IN REF. 1).
SE9ECB03997DB110 CRC64;
                                                               similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 297; DB 1; 26.1%; Pred. No. 1.1e-11;
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                                                               (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROXYISOBUT_DH; 1.
                        methyl-3-oxopropanoate + NADH.
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Mitochondrial
                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1889802; 6430402H10Rik.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD NAD.
PFfam; PP03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
PROSITE; PS00895; 3_HXDROXXISOBUT_DH;
                                                                                                                                                                                                                                                                                                         EMBL; BC003914; AAH03914.1; -. EMBL; AK078175; BAC37162.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 AA; 35440 MW;
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SKKDFSSVFQ 327
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67
208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                           family
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P29266;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Mitochondrial.
-!- TISSUE SPECIFICITY: HIGHER LEVEL IN KIDNEY, LIVER, AND HEART THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96335606; PubMed=8766712;
Hawes J.W., Harper B.T., Crabb D.W., Harris R.A.;
"Structural and mechanistic similarities of 6-phosphogluconate and 3-
"Structural and mechanistic similarities of 6-phosphogluconate and 3-
hydroxyisobutyrate dehydrogenases reveal a new enzyme family, the 3-
Chordata, Craniata, Vertebrata, Euteleostomi;
Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
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K-AA, H.N,R: COMPLETE LOSS OF ACTIVITY.

N-Q: DECREASE IN ACTIVITY.

N-26: DECREASE IN ACTIVITY.
                                                                                                                                                                                                                Rougraff P.M., Zang B., Kuntz M.J., Harris R.A., Crabb D.W.; "Cloning and sequence analysis of a cDNA for 3-hydroxylsobutyrate dehydrogenase. Evidence for its evolutionary relationship to other pyridine nucleotide-dependent dehydrogenases."; J. Biol. Chem. 264:5899-5903(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROGITE: PS00895; 3 HYDROXYISOBUT DH; 1.

Oxidoreductase; NAD; Mitochondrion; Transit peptide.

TRANSIT 1 35 MITOCHONDRION (BY SIMILARIIY).

CHAIN 36 335 3-HYDROXYISOBUTKRATE DEHYDROGENASE.

NP BIND 39 67 NAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bairoch A.;
Unpublished observations (JAN-2001).
-!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CAUTION: Ref.1 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 290; DB 1; Length 335
25.5%; Pred. No. 3e-11;
cive 60; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A32867; A32867.
InterPro; IRPO02204; 3hydroxisobut_dh.
InterPro; IPR006183; 6FGD.
InterPro; IPR006115; 6FGD.
PFam; PF0346; NAD binding_2: 1.
PRINTS; PR00076; 6FGDBDRGNASE.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1
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                                                                                                                                                                         TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J04628; AAAS0312.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methyl-3-oxopropanoate + NADH.-1- SUBCNIT: Nomdimer.
                                                                                                                                                                         STRAIN=Sprague-Dawley; TISSUE=Live
MEDLINE=89174651; PubMed=2647728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frameshift in position 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxyacid dehydrogenases.";
FEBS Lett. 389:263-267(1996).
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208
68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONCEPTUAL TRANSLATION.
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212
335 AA;
                                           Mammalia, Eutheria;
NCBI TaxID=10116;
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TVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFF 426
                                     | | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                             484
                                                                                                                                                                                          198 CGAVGSGQSAKICNNMLLAISMIGTAEAMNLGIRSGLDPKLLAKILNMSSGRCWSSDTYN 257
                                                                                                                                                                                                                                                               485 KCQNILQG-----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQ 539
                                                                                                                                                                                                                                                                                                            258 PVPGVMDGVPSSNNYQGGFGTTLMAKDLGLAQDSATSTKTPILLGSVAHQIYRMMCSKGY 317
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"Utilization of dihydroorotate as sole pyrimidine source by Salmonella
                                                                                                                               LGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDIIN--QGQLASIFLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ELTZ / SGSC1412 / ATCC 700720;
MCDLINE=2154948; PubMed=11677609;
MCDLIBLE=1554948; PubMed=11677609;
MCDLIBLAM, Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florae L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856(2001).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
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Stydene; SG7???; yihU.

InterPro; IPR001204; 3hydroxisobut_dh.

InterPro; IPR00115; 6FGD NAD.

InterPro; IPR00205; 3hyDROXISOBUT DH; 1.

PROSITE; PS00895; 3HyDROXISOBUT DH; 1.

PROSITE; PS00895; 3HyDROXISOBUT DH; 1.

Hypothetical protein; Oxidoreductase; NAD; Complete proteome.

ITI BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
YINU OR STM4023.
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EMBL; AE008887; AAL22862.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           318 SKKDFSSVFQ 327
                                                                                                                                                                                                                                                                                                                                                                                               540 SDNDMSAVYR 549
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16-OCT-2001
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                                                                                                                                         330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG 389
                                                                                                                                                                 64 MLPNGDLVRSVLFGEQGVCETLSREALVIDMSTIHPLQTDNLIADMQSKGFSMMDVPIGR 123
                                                                                                                                                                                                                                                                                                           450 TIAEGLTLAHVTGQSQQTLLDILN-----QGQLASIFLDQKCQNILQGNFKPDFYLKYIQ
                                                                                                                                                                                                             390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin Q., Yuang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=E.coli, STRAIN=K12 / MG1655;
MEDLINE=93347969; PubMed=8146018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
"Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";
"Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flexheri serotype 2a strain 2457T.",
Infect. Immun. 71:2775-2786(2003).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
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       DB 1; Length 298;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                            505 KDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                              10.1%; Score 289.5; DB 1; 25.4%; Pred. No. 2.8e-11; ive 59; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P32142;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypotherical oxidoreductase yinu (EC 1.1.-.)
XIHU OR B3882 OR SF3954 OR S3792.
Escherichia coli, and
                    L Similarity 25.4%; 72; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                  Similarity
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ID YIHU ECOLI
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Query Match
Best Local S:
Matches 72,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLBAPVSG 389
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 LSAEAAVLCEALNLPFDVAVKVMS-GTAAGKGHFTTSWPNKVLSGDLSPAFMIDLAHKDL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                          EMBL) A40826; S40826.
ECGENE; BG11847; YihU.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6FGD_NAD.
Fram; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 26.4%; Pred. No. 3.7e-11; nes 74; Conservative 54; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             74FBC8C09FA7881C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508 RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GIALDVANQLHVPMPLGAASREVYSQARAAGRGRQDWSAI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.0%; Score 287.5; DB 1 26.4%; Pred. No. 3.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 AA.
                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein, Oxidoreductase, NAD, ACT SITE 171 171 BY SIMILARITY
                                                                                                                                                                    EMBL; L19201; AAB03015.1; -.
EMBL; AE000464; AAD13444.1; -.
EMBL; AE015402; AAN45389.1; -.
                                                                                                                                                                                                                                 AE016990; AAP18811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              171 171 B
298 AA; 31158 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                              ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                               EMBL;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 GARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADIVT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :: :||:| :||:| | : ||:| | :|| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Ghein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 SFAAVCSRSV-ASKTP----VGFIGLGNMGNPMAKNLMKHGYFLIIYDVFPDACKEFQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005739; C:mitochondrion; NAS.
GO; GO:0006442; F:3-hydroxyisobutyrate dehydrogenase activity; NAS.
GO; GO:0006573; P:valine metabolism; NAS.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; GFGD.
InterPro; IPR006115; GFGD.
Pfam; PF03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methyl-3-oxopropanoate + NADH.
-- subuntr: Homodimer (By similarity).
--- suburtr: Homodimer (By similarity).
--- SUBCELLULAR LOCATION: Mitcochondrial.
--- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94147969; PubMed=8313870;
Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
Tissot J.-D., Barioch A., Appel R.D., Hochstrasser D.F.;
"Human liver protein map: update 1993.";
Electrophoresis 14:1216-1222(1993).
-: CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-HYDROXYISOBUTYRATE DEHYDROGENASE. NAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%; Score 281; DB 1; Length 336; 26.4%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 32-336 FROM N.A.
Du F., Wohldmann P., Holmes A.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DA3128774A91AF48 CRC64;
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Oxidoreductase; NAD; Mitochondrion; Transit peptide.
TRANSIT 1 36 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, BC032324; AAH32324.1; -
EMBL, AC007130; -; NOT ANNOTATED_CDS.
SWISS-2DPAGE; P31937; -HUMAN.
Siena-2DPAGE; P31937; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35329 MW;
                                                                                                                                                                                                                                                                                                                                           cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC: 4907; HIBADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
209
336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 37-47.
                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236795; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GK; P31937
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ACT SITE
SEQUENCE
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RA MEDINESCUS GOOG, PUNDECHED 7312;

RA MEDINESCUS GOOG, PUNDECHED 7312;

RA MEDINESCUS GOOG, SCHORER S.E. LIDEN, Hoskins R.A., Galle R.F.,

SUCCOR G.G., Northan J.R., Yandell M.D., Shburner M., Henderson S.N.,

Suction G.G., Worthan J.R., Yandell M.D., Shburner M., Henderson S.N.,

RA BERING R.C., BOXTCH E.G., Helt G., Champe M., Pfeiffer B.D.,

RA BERING R.C., BOXTCH E.G., Helt G., Nelson C.R., Mixlos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA BERSON K.Y., Borchan M.R., Bowck J., Brokstein P., Brottier P.,

RA BOCKAN D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA BOKKAN D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA GLANC C., Busam D.A., Danike C., Davenport L.B., Davies P.

RA GLANC R., Dough L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA BALDS B., Lolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA BALDS B., Delcher A., Deng S., Gelbart W.M., Glasser K.,

Godson K., Dough L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harrish M.,

RA Harrish N.J., Harvey D.A., Heinan T.J., Hernandez J.R., Houck J.,

RA Jalain M. Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Harrish N.J., Harvey D.A., Heinan T.J., Hernandez J.R., Morenten D.,

RA Liu X., Mattell B., McIntosh T.C., Moreod M.P., Morberson D.,

RA Liu X., Mattell B., McIntosh T.C., Moreod M.P., Norberson D.,

RA Houston D.R., Wobarry C., Morris J., Moshrefi A.,

RA Berkulov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A.,

RA Berkulov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A.,

RA Berkulov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A.,

RA Berkulov G., Milshina N.V., Nobarry C., Siden-Kiamos I., Smith T.,

RA Berkulov G., Wilshina W., Nurphy B., Murphy L., Murzhy D.M., Neissenbach J.,

RA Berkulov G., Wilshina S., Nobarry C., Siden-Kiamos I., Shimpson M., Strong R., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA B
           ELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGE 429
                                                   142 ELAKEVEKMGAVFMDAPVSGGVGAARSGNLTFMVGGVEDEFAAAQELLGCMGSNVVYCGA 201
                                                                                                430 VGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILN--QGQLASIFLDQKCQ 487
                                                                                                                                           202 VGTGQAAKICNNMLLAISMIGTAEAMNLGIRLGLDPKLLAKILNMSSGRCWSSDTYNPVP 261
                                                                                                                                                                                        488 NILQG-----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDN 542
                                                                                                                                                                                                                    262 GVMDGVPSANNYQGGFGTTLMAKDLGLAQDSATSTKSPILLGSLAHQIYRMMCAKGYSKK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable 3-hydroxy;sobutyrate dehydrogenase, mitochondrial precursor (BC 1.1.1.31) (HIBADH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 AA
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MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [6-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                | |:|::
322 DFSSVFO 328
                                                                                                                                                                                                                                                                                    543 DMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9V8MS; Q9V8M6;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTABKCDLFIQEGARLGRTPAEVVSTCDIT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 FACVSD---PKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECMGKKITHCGVYGMGQAAĞLCNN7MLAISMIGVSEAMNLA
VRGGLDANVE -> KROĞRENVHQGBDHPINAKUHMGPGRQ
AVQQHDAGILLDDRCFGGHESGGAPGSRCQLIRRDHQLLHRT
LLGLGDLQPCARSLPQCPSQQGLRRRFLLGSDHQGSGSGGLR
                                                                                                   MEDLINE=22426669; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
NAIVDASYDEMTADGVNKDTIFIDSSTISPDLVKSLQKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKGARFIDAPVSGGVPGAEQATLTFMVGGTEAEYNAVKAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Biol. 3. RESEARCH0083.1-RESEARCH0083.22 (2002).
-!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9V8MS-2; Sequence=VSP 001281, VSP 001282; SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCORFOLTHPAGISGAOGLPVAVR (in isoform
                                                                                                                                                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBGN004390; CG15093.
InterPro; IPR0061399; Bydroxisobut_dh.
InterPro; IPR006139; 6PGD.
InterPro; IPR006139; 6PGD.
InterPro; IPR006115; 6PGD. NAD.
Pfam; PF03446; NAD bindaing_2; 1.
PRINTS; PR00076; 6FGDHDKGNASE.
Hypothetical protein; Oxidoreductase; NAD; Mitochondrion; Transit peptide; Alternative Splicings; TRANSIT.

TRANSIT 125 MITOCHONDRION (RV STMILADITWAY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROBABLE 3-HYDROXYISOBUTYRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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/FIId=VSP 001282.
A39B534753EAE83E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity)
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAD (ADP PART) (POTENTIAL).
"The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No 1.5e-10; 47; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTIG=VSP 001281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9V8M5-1; Sequence=Displayed;
                                                                               AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003798; AAF57638.2; -. EMBL; AE003798; AAM68444.1; -.
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324
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196
227
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                                                                                                                                                                                                                                                                                                                                                                  systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228
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196
95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Long;
                                                                                                                                                                                                                                                                                                          Lewis S.E.;
                                                                            REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT SITE
VARSPLIC
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us-10-067-482-2.rsp

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Oxidoreductase; NAD; Complete proteome
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                                                                                                                           445 GSFMATIAEGLILAHVTGQSQQTLLDILNQGQLASIFLDQKC----QNILQG----- 492
                                                      APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQ 444
                                                                                       144 APVSGGVPGAEQATLTFMVGGTEAEYNAVKAVLECMGKKITHCGVYGMGQAAKLCNNMML 203
                                                                                                                                                         204 AISMIGVSEAMNLAVRQGLDANVFAEIINSS-----TGRCWASEIYNPVPGVCPSAPA 256
 MEDLINE-Z0437337; PubMed=10984043; Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Gollty L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steele M.I., Lorenz D., Hatter K., Park A., Sokatch J.R.; "Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding methylmalonate-semialdehyde dehydrogenase and 3-
                                                                                                                                                                                                   --NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- INDUCTION: By valine.
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
10-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methyl-3-oxopropanoate + NADĤ.
-!- PATHWAY: Distal valine metabolic pathway.
                                                                                                                                                                                                                                                                                                                               298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AR004778; AAG66957.1; -.
PIR; C42902; C42902.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6FGD_NAD.
Pfam; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3_HYDROXXISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydroxyi sobutyrate dehydrogenase.";
J. Biol. Chem. 267:13585-13592(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-92317087; PubMed=1339433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M84911; AAA25892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEOUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                          270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADIVTELAQVIVSRGGRFLEAPVSG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GVGGARAĞTLSFIVGGPAEGFARARPVLENMGRNIFHAĞDHĞAĞQVAKICNNMLLĞILMA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 TIAEGLILAHVTGQSQQTLLDILNQ---GQLA-----SIFLDQKCQNILQGNFKPDF 498
                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                            4 IAFLGLGNMGGPMAANLLKAGHRVNVFDLQPKAVLGLVEQGAQGADSALQCCEGAEVVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::|||||:::||||241 -VRLMNKDLGIALANAQAVQASTPLGALARNLFSLHAQADAEHEGLDFSSIQKLY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 YLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDN--DMSAVYRAY 551
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SUMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                        17;
                                                                                                                                               Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial
(EC 1.1.1.31) (HIBADH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WormPep; B0250.5; CE18481.
InterPro; IPR002204; 3hydroxisobut dh.
SROSITE; PS00895; 3. HYDROXYISOBUT DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
NP_BIND 2 30 NAD (ADP PART) (POTENTIAL).
                                                                                                                                           ; Score 261.5; DB 1; Length
; Pred. No. 1.6e-09;
51; Mismatches 151; Indels
NAD (BY SIMILARITY).
BY SIMILARITY.
0C4D7B5A7C870730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA
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EMBL; AL031630; CAA21003'1; -.
EMBL; 281453; CAA21003.1; JOINED.
PIR; T18682; T18682.
                                                                             298 AA; 30486 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z81453; CAB03798.1; -.
                                                                                                                                                      9.1%;
                                                                                                                                                                                             Local Similate,
nes 76; Conservative
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                                              171
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                                                                                                                                                                                         Similarity
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                                                                                                        271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFAC 330
                                                                                                                                                                    331 VSDPKAAKDIVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGN 390
                                                                                                                                                                                                          124
                                                                                                                                                                                                                                   ----QQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGS 446
                                                                                                                                                                                                                                                      125 VIGAQQAT---LIFMVGAGNDATFKRAEAVLSLMGKNIVNLGAVGNGTAAKICNNMLLGI 181
                                                                                                                                                                                                                                                                                             447 FWATIAEGLTLAHVTGQSQQTLLDILN-------QGQLASIFLDQKCQNILQ 491
                                                                                                                                                                                                                                                                                                                          182 OMVAVAETMNLGISMGLDAKALAGİVNTSSGRCWSSDTYNPVPGVIENİ---PSCRGYAG 238
                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                        492 GNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYK-RAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-i-SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                  31;
                                                 Score 259.5; DB 1; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000357; AAC757781; -.
PIR; D65054; D65054.
ECOGENE; EG13104; ygbJ.
InterPro; IPR002204; 3hydroxisobut dh.
PROSTIE; P80895; 3 HYDROXYISOBUT DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
ACT_SITE 178
                                                                             48; Mismatches 143; Indels
 172 PROBABLE.
31217 MW; F30B423A597CABF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09E94256EDDFC26C CRC64;
                                                                  2.1e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase ygbJ (EC 1.1..-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AA.
                                                                  Pred. No.
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MEDLINE=97426617; PubMed=9278503;
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                                              9.1%;
                                                             25.8%;
                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                299 AA;
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                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
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                                        Query Match
Best Local Simil
Matches 77; (
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Length 302;

8.3%; Score 239; DB 1;

Query Match

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                                                                                                                                                                                                                                                                                                       61 AEKLDALLVLVVNAAQVKQVLFGETGVAQHLKPGTAVWVSSTIASADAQEIATALAGFDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 HQLLAGVHIAAGAEAMALAARAGIPLDVMYDVVTNAAGNSWMFENRMRHVVDGDYTPHSA 240
                                                                                                                                                  321 VSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGG
                                                                                                                                                                                                                                                                                                                                                                                                    381 RFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLG-EVGNAAKMMLI
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MEDLINE=2206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J.A., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Praser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE-98255987, PubMed-5634230,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH) MMSB OR RV0751C OR MT0775 OR MTV041.25C OR MB0773C, Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 VDIFVKDLGLVADTAKALHFPLPLASTALNMFTSASNAGYGKEDDSAVIKIF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 LKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                      Indels
22.9%; Pred. No. 4.1e-08; ive 64; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.tuberculosis; STRAIN=H37Rv;
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                              67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium bovis.
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 MLPTGEVVRRCY---TDVLAAARPATLFIDSSTISVTDAREVHALAESHGMLQLDAPVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 TIAEGLTLAHVTGQSQQTLLDIINQGQLASIFLDQKC-----QNILQGNFKPDFYLKY
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                                                                     methyl-3-oxopropanoate + NADH.
PATHWAY: Distal valine metabolic pathway.
SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                          ., Nařl. Acad. Sci. Ú.S.A. 100:7877-7882(2003).
CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547
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BY SIMILARITY.
       complete genome sequence of Mycobacterium bovis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.2%; Score 234.5; DB 1; Best Local Similarity 26.0%; Pred. No. 7.6e-08; Matches 74; Conservative 39; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase yfjR (EC 1.1.-.-)
PHYR OR BSU07990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002204; 3hydroxisobut dh. PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1. Oxidoreductase; NAD; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL021958; CAA17518.1; -. EMBL; AE006969; AAK45016.1; -. EMBL; BX248336; CAD93635.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29679 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculist; Rv0751c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168
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TIGR; MT0775; -.
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                                                                                                                                                                                                                                  REDELINE-98044033; PubMed=9384377;

KUNDELINE-98044033; PubMed=9384377;

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Derriso R., Bourschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterboft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Pabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Haicot J., Harwood C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Haga K., Haicot J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Medina N., Wellado R.P., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Wellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,

RA Noone D., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Prescan E., Pujic P., Purnelle B., Ropoport G., Rey M., Reynolds S.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Seriotti A., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Viari A., Wambutt R., Wander E., Wedler H., Wannier P., Shin B.S.,

RA Viari A., Wambutt R., Wander E., Wedler H., Yamane K., Yashilus H., Pubrchiu Bacillus

RY Subrilse P., Wander S., Vondenbol M., Vannier P., Shin B.S., Salver P., Shin P.S., Vannielle R., Wedler E., Wedler H., Yamane C., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zonstein E., Yoshikawa H.F., Zonstein E., Yoshikawa H.F., Zonstein E., Yoshikawa H.F., Zonstein E., Yoshikawa H.F., Zonstein E., Yoshikawa H.F., Yoshikawa H.F., Zumstein E., Yoshikawa H.P., Zonstein E., Yoshikawa H.P., Zonstein E., Yoshikawa H.F., Zonstein E., Yoshikawa H
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-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
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Subtilist; BG12914; YfjR.
Interpro; IPR002204; 3hydroxisobut_dh. ALSE NEG.
PROSTIE; PS00895; 3 HYDROXISOBUT DH; FALSE NEG.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
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4.9%; Pred. No. 2.8e-07;
ve 51; Mismatches 133; Indels
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for trehalose metabolism and acetoin utilization."; Microbiology 142:3057-3065(1996).
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EMBL; D78509; BAA24303.1; -.
EMBL; Z99108; CAB12628.1; -.
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121 AKPLLDSLSQQIFDVGEESKTANAAK--ISINFLLVSMLEALSESFLMMEKYGLEQKQFL 178
                                                         470 DILNQGQLASIFLDQKCQN----ILQGNFKP-DFYLKYIQKDLRLAIALGDAVNHPTPMA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98295897; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cordon S.V., Biglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy I., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Ragers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nolson W.C. Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase Rv0770/MT0794 (EC 1.1.-.-).
RV0770 OR MT0794 OR MTCY369.15.
                                                                                                                                                                                                                                                         295 AA
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                                                                                                                                       234 ELAKSHFESGIEKGFGDLDWAALIK 258
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                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                     STANDARD;
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InterPro, IPR002204; 3hydroxisobut_dh. PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1. HYDothetical protein; Oxidoreductase; NAD; Complete proteome. ACT_SITE 176 176 BY SIMILARITY.

Tuberculist; Rv0770; -.

BY SIMILARITY.
7A9E7FBFAD0E95B8 CRC64;

295 AA; 30445 MW;

ACT SITE SEQUENCE

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                                                                                                                                                                                       265 PIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTC 324
                                                                                                                                                                                                                                                                                                                                                                          325 DITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
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                                                                                                                                                                                                                                            | ::||| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: |
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                                                                                                               25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINERG / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed=7542800;
Helischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kellay J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Ruhrmann J.L., Geoghagen N.S.M., Wenter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria, Gammaproteobacteria, Pasteurellales;
Pasteurellaceae; Haemophilus.
                   Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6PGD NAD.
Pfan: PF03446; NAD_binding_2; 1.
PR031TE; PS00895; 3 HYDROXYISOBUT DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 NFKPDFYLKYI----QKDLRLAIALGDAVNHPTPMAAAA 527
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                   DB 1;
                                                     24.7%; Pred. No. 2.8e-06; ive 48; Mismatches 137;
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase HII010 (EC 1.1.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AA
              7.3%; Score 209.5;
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                                                                                                69; Conservative
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                                 Similarity
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Query Match
Best Local
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                                                                                           Matches
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X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Xonno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Coniwa H.,

Radota K., Matsudi F., Sissi C., King B., Kochiwa H.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo M., Anno H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Barconstein M.J., Bult C., Fletcher C., Fuljia M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fuljia M., Gariboldi M.,

A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
                                                                                                                                                                                                                    447
                                                                                                  270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGAR-LGRTPAEVVSTCDITF 328
                                                                                                                                                                                   68 ILVVNAAQANAVLFGENGIAKKLKAGTAVMVSSTMAAQDAQIISQKLTELGLIMLDAPVS 127
                                                                                                                                                                                                                                   507
                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                  GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLG-EVGNAAKMMLIVNMVQGSF
                                                                                                                             8 VAVIGLGSMGMGAAVSCINAGLTTYGIDLNPVALEKLKAAGAKAVAANGYDFAHELDAVV
                                                                                                                                                           329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                          MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97445118; PubMed=9299445;
Izumoto Y., Kuroda T., Harada H., Kishimoto T., Nakamura H.;
Irepatoma-derived growth factor Dellongs to a gene family in mice
showing significant homology in the amino terminus.";
Biochem. Biophys. Res. Commun. 238:26-32(1997).
                                                                          ..
                                            Length 301;
                                                                                                                                                                                                                                                                                                                                                    248 GLVNDTAKSLHFPLHLASTAYSMFTEASNAGYGKEDDSAVIKIF 291
                                                                                                                                                                                                                                                                                                                                    508 RLAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                            ; Score 198; DB 1; Length 30; Pred. No. 1.5e-05; 62; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning of novel gene related to thymus development."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                 7C615A25B0947D18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      P51859; Q9CYA4; Q9JK87;
01-0CT-1996 (Rel. 34, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatoma-derived growth factor (HDGF)
HDGF OR IDRM1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Testis;
                    31035 MW;
                                               6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao Y., Chen W., Wang Y.; "Cloning of novel gene rel
                                                                             59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
       177 1
301 AA;
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                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
        ACT SITE
SEQUENCE
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                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 RLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                      Hayashizaki Y., "Hayashizaki Y.," "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.5%; Score 186.5; DB 1; Length 237; 29.8%; Pred. No. 5.8e-05;
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P -> H (IN REF. 1).
Q -> P (IN REF. 1).
AAE4CF574DA4733F CRC64;
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Growth factor; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF251787, AAF65469.1; --
EMBL, AK017863; BAB30979.1; --
EMBL, BC005713; AAH05713.1; --
EMBL, BC021654; AAH21654.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26269 MW;
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InterPro; IPR000313; PWWP
Pfam; PF00855; PWWP; 1.
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190
229
                                                                                      Nature 409:685-690(2001)
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118 1
190 1
229 2
237 AA;
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Matches 6
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STANDARD;
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       HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                          KEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDEK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415
                                 70 KEKFGKPNKRKGFSEGLWEIEN----NPTVKASGYQSSQKKSCAAEPEVEPEAHEGDGD 124
                                                                    127 RKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKR----AQEQSPRKRGRPPK----D 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 CFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQG 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 TVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYE-----DCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gordon E.H.J., Pike A.D., Hill A.E., Cuthbertson P.M., Chapman S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification and characterization of a novel cytochrome c3 from Shewanella frigidimarina that is involved in Fe(III) respiration."; Biochem. J. 349:153-158(2000).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                              28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase in cytochrome c3 5'region (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.5%; Score 185.5; DB 1; Length 194; 26.3%; Pred. No. 5.2e-05; Live 45; Mismatches 81; Indels 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 AA; 20865 MW; 4B4236749F1E8701 CRC64;
                                                                                                                                        178 EKDLTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                              194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                           Alteromonadaceae; Shewanella.
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                                                                                                                                                                                                                                                                                                                                                                      Sĥewanella frigidimarina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 26.3:
es 51; Conservative
                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NCIMB 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10861223;
                                                                                                                                                                                                                                                                 SHEFR
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RESULT 21 HDGF_HUMAN

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                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2096 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hepatoma-derived growth factor (HDGF) (High-mobility group protein 1-
                                                                                                                                                                                                         Nakamura H., Izumoto Y., Kambe H., Kuroda T., Mori T., Kawamura K., Yamamoto H., Kishimoto T., "Molecular cloning of complementary DNA for a novel human hepatomaderived growth factor. Its homology with high mobility group-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Heparin-binding protein, with mitogenic activity for
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 300043; -. Gytoplasm; TAS. GO; 6000573; C: cytoplasm; TAS. GO; 60: 0005615; C: extracellular space; TAS. GO; GO: 0008201; F: heparin binding; TAS. GO; GO: 0008283; P: cell proliferation; TAS. InterPro: IRRO00313; PWWP, domain. PF00855; PWWP; 1. SMART; SM00293; PWWP; 1. PROSITE; PS50812; PWWP; 1.
                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 4-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Contains 1 PWWP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                            Biol. Chem. 269:25143-25149(1994).
                                                                                                                                                                                 TISSUE=Hepatoma;
MEDLINE=95014294; PubMed=7929202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC018991; AAH18991.1; -.
PIR; A55055; A55055.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci.
                                                                                                     Homo sapiens (Human)
                                                                           like 2) (HMG-1L2).
HDGF OR HMG1L2.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=9606;
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8
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                                                                                                                                                                                                                                                                                                                             KEKFGKPNKRKGFSEGLWEIEN----NPTVKASGYQSSQKKSCVEEPEPEPEAAEGDGD 124
                                                                                                                                                                                                                                                                                                                                                                                                              KK-GNAEGSSDE---EGKLVIDEPAKEKNEKGALKRRAGDLLEDSPKRPKEAENPEGEE- 179
                                                                                                                                                                                               99
                                                                                                                                                                                                                                       69
                                                                                                                                                                                               7 RLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAH
                                                                                                                                                                                                                        RKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQ----EQSPR--KRGRPPKDEKD
                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT GLY-39.
Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,
Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D.,
Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95327934; PubMed=7604265; Palonbo F., Gallinari P., Iaccarino I., Lettieri T., Hughes M., Palong O., Hsuan J.J., Jiricny J.; Truong O., Hsuan J.J., Jiricny J.; Truong O., Hsuan Gibs., Gibs., a 160-kilodalton protein essential for mismatch-binding activity in human cells.";
                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97098445; PubMed=8942985;
Acharya S., Wilson T., Gradia S., Kane M.F., Guerrette S.,
Maraischky G.T., Kolodner E.D., Fishel R.;
"hMSH2 forms specific mispair-binding complexes with hMSH3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSH6 HUMAN STANDARD; PRT; 1360 AA.
P52701; 043706; 043917; QBTCX4;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
DNA mismatch repair protein MSH6 (Muts-alpha 160 kDa subunit)
                                                                                                              DB 1; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=98116665; PubMed=9455487;
Shiwaku H.O., Wakatenki S., Mori Y., Fukushige S., Horii A.;
"Alternative splicing of GTBP in normal human tissues.";
DNA Res. 4:359-362(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-116 FROM N.A., AND VARIANT GLY-39.
MEDLINE=96435440; PubMed=8838326;
Nicolaides N.C., Palombo F., Kinzler K.W., Vogelstein B.,
                                                                                                                                                      Indels
                                                                 26788 MW; DD60D9203BDD4B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 69-1360 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 93:13629-13634(1996).
                                                                                                                                                      30; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KEAATLEVERPLPMEVEK-NSTPSEPGSGRGP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GTMBP) (P160).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIIPESSTVKGMMAGPMAAFKWQPIASEPVKDADP 215
                                                                                                            6.5%; Score 185.5; DB 1
29.8%; Pred. No. 6.8e-05;
                                               POLY-GLU
  Growth factor; Heparin-binding.
DOMAIN 12 69 PWWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mismatch binding protein) (GTBP) MSH6 OR GTBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268:1912-1914 (1995).
                                                                                                                                                         64; Conservative
                                             223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                   240 AA;
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                        SEQUENCE
                                                                                                            Query Match
Best Local
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MEDLINE=95127935; PubMed=7664266; Papadopoulos N., Nicolaides N.C., Liu B., Parsons R., Lengauer C., Palombo F., D'Arrigo A., Markowitz S., Willson J.K.V., Kinzler K.W., Jiricny J., Vogelstein B.; The Markowitz S., Willson J.K.V., Kinzler K.W., Mutations of GTBP in genetically unstable cells."; Science 268:1915-1917(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Association of hereditary nonpolyposis colorectal cancer-related tumors displaying low microsatellite instability with MSH6 germline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyaki M., Konishi M., Tanaka K., Kikuchi-Yanoshita R., Muraoka M.,
Yasuno M., Igari T., Koike M., Chiba M., Mori T.,
"Germline mutation of MSH6 as the cause of hereditary nonpolyposis
                                                                                                                                                                                    Drummond J.T., Li G.-M., Longley M.J., Modrich P.; "Isolation of an hMSH2-pl60 heterodimer that restores DNA mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS CRC ILE-285; ARG-566; GLY-803 AND THR-1087, AND VARIANTS GLY-39; ASP-220; VAL-396 AND LEU-800.
MEDLINE=20005667; PubMed=10537275;
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Wang Q., Lasset C., Desseigne F., Saurin J.-C., Maugard C.,
Navarro C., Ruano E., Descos L., Trillet-Lenoir V., Bosset J.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu Y., Berends M.J.W., Mensink R.G.J., Kempinga C., Sijmons R.H.,
van Der Zee A.G.J., Hollema H., Kleibeuker J.H., Buys C.H.C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gupta R.D.,
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Plaschke J., Krueger S., Pistorius S., Theissig F., Saeger H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       щ
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hMSH6 genes in 75 French kindreds with nonpolyposis colorectal
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                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20245492; PubMed=10783165;
Wang Y., Cortez D., Yazdi P., Neff N., Elledge S.J., Qin J.;
"BASC, a super complex of BCR1-associated proteins involved
recognition and repair of aberrant DNA structures.";
Genes Dev. 14:927-939(2000).
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"Molecular cloning of the N-terminus of GTBF."; Genomics 31:395-397(1996).
                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION OF MSH6 AS MEMBER OF BASC.
                                                                                                                     CHARACTERIZATION, AND PARTIAL SEQUENCE
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MEDLINE=99452590; PubMed=10521294;
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                                                                                                                                                        PubMed=7604264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Genet. 17:271-272(1997).
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                                                                                                                                                                                                                                                                      repair to tumor cells.";
Science 268:1909-1912(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colorectal cancer.";
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                                                                                                                                                            MEDLINE=95327933;
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Length 1360;

DB 1;

0.14;

5.2%; Score 148.5; 9.9%; Pred. No. 0.1

19.9%;

U73733; AAB47425.1; JOINED. U73734; AAB47425.1; JOINED. U73736; AAB47425.1; JOINED. BAA23674.1;

D89645;

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BAA23674.1; JOINED.
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BAA23675.1;
  BAA23674.1;
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                                                                                                              Similarity
                             D89640; I
                                                D89643;
D89644;
                    D89639;
                                                                     D89646;
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          D89638;
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Best Local
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                                                                                                                                                                                                     SUBUNIT: Heterodimer of MSH2 and MSH6 (GTBP). Part of the BRCAl-sasociated genome surveillance complex (BASC), which contains BRCAl, MSH2, MSH6, MLH1, ATM, BLM, PMS2 and the RADSO-MREII-NBS1 protein complex. This association could be a dynamic process Subcetiullar incomplex contains subcetiullar incomplex. The cell cycle and within subnuclear domains. ALTERNATIVE PRODUCTS:
       and sporadic
"Involvement of hMSH6 in the development of hereditary and sporadic colorectal cancer revealed by immunostaining is based on germline mutations, but rarely on somatic inactivation.";

Int. J. Cancer 97:643-648 (2002).

-I-FUMCITOR. Restores repair of base-base and single- nucleotide insertion-deletion mismatches, and increases the proficiency to process heteroduplexes with two-, three-, or four- nucleotide insertion-deletion mismatches. GTBP binds covalently to G/T
                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                        IsoId=P52701-1; Sequence=Displayed;
                                                                                                                                                                                               Name=GTBP-alt;
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                                                                                   mismatches.
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37;
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|153 GSKSK--EAQKGGHFYSAKPEILRAMQRADEAINKDKIKRLELAVCDEPSEPEEEEMEV 210
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28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
              239;
         Indels
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89; Mismatches 234;
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                                                                                                                                                                                                                               "J Bacteriol. 176:3126-3139(1994).

J. Bacteriol. 176:3126-3139(1994).

J. CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.

J. PATHMAX: Haxces monophosphate shunt.

J. PATHMAX: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                               ij.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                            "Cloning and analysis of duplicated rfbM and rfbK genes involved the formation of GDP-mannose in Escherichia coli 09:K30 and participation of rfb genes in the synthesis of the group I K30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                              Dodgson C., Kido N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%; Score 146; DB 1; Length 468; 22.7%; Pred. No. 0.049; tive 51; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIGURES, TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP. SEQUENCE 468 Aa; 51625 MW; C13D94CFD78BFF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 EAPVSGNOOLSNDGMLVI---LAAGDRG------
                                                                                                                          Jayaratne P., Bronner D., Maclachlan R.P., Whitfield C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PMAAAANEVYKR 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR008927; 6DGDH_C_like.
Interpro; IPR006183; 6PGD.
Interpro; IPR006114; 6PGD_dcarbox.
Interpro; IPR006113; 6PGD_dcarbox.
Interpro; IPR006115; 6PGD_NAD.
Interpro; IPR006118; 6PGDOM_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03446; NAD binding 2; 1. PRINTS; PR00076; 6PGDHDRGNASE.
                                                                            SEQUENCE FROM N.A.
STRAIN=09:K30:H12 / E69;
MEDLINE=94252978; PubMed=7515042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L27646; AAA21136.1; -.
PIR; I41250; I41250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 22.7%
Matches 73; Conservative
                                                                                                                                                                                                                       capsular polysaccharide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00393; 6PGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00349; 2PGD
                                            NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98050922; PubMed=9390556; MEDLINE=98050922; PubMed=9390556; Medelmann W., Yang K., Umar A., Heyer J., Lau K., Fan K., Liedtke W., Cohen P., Kane M.K., Lipford J.R., Yu N., Crouse G.F., Pollard J.W., Kunkel T., Lipkin M., Kolodner R., Kucherlapati R.; F., Whateion in the mismatch repair gene Msh6 causes cancer susceptibility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                       "CDNA sequence, map, and expression of the murine homolog of GTBP, DNA mismatch repair gene."; Genomics 36:288-295(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 375-425 AND 1001-1050 FROM N.A.

Donohue P.J., Feng S.L.Y., Alberts G.F., Guo Y., Peifley K.A.,

Bun D.K.W., Winkles J.A.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Restores repair of base-base and single- nucleotide

insertion-deletion mismatches, and increases the proficiency to

process heteroduplexes with two., three-, or four- nucleotide

process heteroduplexes with two., three-, or four- nucleotide

insertion-deletion mismatches. GTBP binds covalently to G/T
                                                                                       (G/T)
                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Heterodimer of MSH2 and MSH6 (GTBP).
SIMILARITY: Belongs to the DNA mismatch repair mutS family.
SIMILARITY: Contains 1 PWWP domain.
                                                                                                                                                                                                                                                                          я
Н
   WSH6_MOUSE STANDARD; PRT; 1358 AA.
P554276, 054710;
01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA mismatch repair protein MSH6 (MutS-alpha 160 kDa subunit)
mismatch binding protein) (GTBP) (GTMBP) (P160).
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=96411686; PubMed=8812455;
Corradi A., Croci L., Stayton C.L., Gulisano M., Boncinelli
Consalez G.G.;
1358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF031087; AAB88445.1; -. AF031085; AAB88445.1; JOINED. AF031086; AAB88445.1; JOINED.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000432; Muts_C.
InterPro; IPR000432; Muts_II.
InterPro; IPR007866; Muts_III.
InterPro; IPR007861; Muts_III.
InterPro; IPR007861; Muts_IV.
InterPro; IPR0070313; PWWP_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U61388; AAB39930.1; -. U61389; AAB39931.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF01624; MutS_I; 1.
Pfam; PF05188; MutS_II; 1.
Pfam; PF05192; MutS_III; 1.
Pfam; PF05190; MutS_III; 1.
Pfam; PF00488; MutS_V; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U42190; AAC53034.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 91:467-477(1997).
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/0la;
                                                                                                                                   OR GIMBP
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485 AA; 53102 MW;
                                           EMBL; Y17297; CAA76734.1; -. HSSP; P00349; 2PGD.
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                                                                                                                                                                                                          Best Local Similarity 22.79
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella pneumoniae.
                                                                                                                      Pfam; PF00393; 6PGD;
                                                                                                                                 Pfam; PF03446; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Chedid;
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                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                             |||||| |: || || : || || : :|| GDLVWARCHGGYBWWPCLVYNNPFDGTFIRKKGKSVRVHVQFFDDSFTRGWVSKRMLKPYT 152
                                                                                                                                                                                                                                                                                        153 GSKSK--EAQKGGHFYSSKSEILRAMORADEALSKDTAERLQLAVCDEPSEPEEEEFFEV 210
                                                                                                                                                                                                                                                                                                            H----NSSDDKNRRNSSEERSRPNSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSK 157
                                                                                                                                                                                                                                                                           ------KGKDQTSS 101
                                                                                                                                                                                                                                                                                                                        211 HEAYLSDKSEEDNYNESEEAQPSVQGPRR----SSRQVKKRRVISDSESDIGGSDVEFK 266
                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                 9 GDLVWGKLGRYPPWPGKIVNPPKD--LKKPRGKKC-FFVKFF-GTEDHAWIKVEQLKPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    0560077;
16-0CT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (BC 1.1.1.44).
                                                                                                                                                                                               DB 1; Length 1358;
                                                                                                                           N -> T (IN REF. 2).
Y -> D (IN REF. 2).
S -> N (IN REF. 2).
C -> Q (IN REF. 2).
G -> E (IN REF. 2).
W, 2031F78D477804AD CRC64;
                                                                                                                                                                                                                89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Zygomycota, Zygomycetes, Mucorales,
Cunninghamellaceae, Cunninghamella.
                                                                                               ATP (FOTENTIAL).
DG -> EA (IN REF. 2).
QK -> PE (IN REF. 2).
N -> T (IN REF. 2).
Y -> D (IN REF. 2).
                                                                                                                                                                                                                                                                       65 AHKEEMIKINKGKRFQQAVDAVEEFLRRA------
                                                                                                                                                                                            5.1%; Score 145.5; DE 24.0%; Pred. No. 0.22; tive 29; Mismatches
Pfam; PF00855; PWWP; 1.
ProDom; PD001263; MutS_C; 1.
SWART; SM00534; MUTSac; 1.
SWART; SM00533; MUTSd; 1.
SWART; SM00593; PWWP; 1.
PROSITE; PS00486; DNA MISMATCH REPAIR_2; 1.
PROSITE; PS00812; PWWP; 1.
                                                                             PWWP.
POLY-GLU.
                                                                  DNA repair; ATP-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                   SPLKRAQEQSPRKRGRPPKDEKDL 181
                                                                                                                                                                                                                                                                                                                                                                     267 PDTKQEGSSDDASSGVGDSDSEDL 290
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                                                                                                                                                                          1358 AA; 151075
                                                                                                                                                                                                     Local Similarity 24.09
                                                                                                         99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cunninghamella elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4853;
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374
754
800
1227
1329
1333
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                                                                                    DOMAIN
NP BIND
CONFLICT
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CONFLICT
CONFLICT
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6PGD_CUNEL
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     and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 CVSDPKAAKDLVLGPSG-----VLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | :: | :: | 64 CAKLKRPRKVMLLVKAGSAVDAFIDQLLPHLBEGDIIIDGGNSHFPDSIRRTKELEAKGI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 RFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTS-----FFLGEVGNA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 AKWALIVNMVQGSFMATIAEGLTLAHV-TGQSQQTLLDIL---NQGQLASIFLDQKCQNI 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obta M,

"Genomic organization of the Klebsiella pneumoniae cps region
responsible for serotype K2 capsular polyeaccharide synthesis in the
virulent strain Chedid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 LOGNEKPDEYLKYIQKDLRLAIALG------DAVNHPTPMAAAANEVYKR 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 LR--FKDTDGQPLVTKIRDTAGQKGTGKWTAIDSLDRGIPVTLIGEAVYSR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P41576; Q44461; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 28-FBB-2003 (Rel. 34, Last annotation update) 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95204345; PubMed=7896702;
Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.0%; Score 143.5; DB 1; Length 22.7%; Pred. No. 0.074; tive 50; Mismatches 140; Indels
     Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F7E6DDFF3D21EFB2 CRC64;
modified and this statement is not removed. entities requires a license agreement (See h
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                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PRO0076, 6 FGDHDRGNASE.
TIGRFAMS, TIGR00873, gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
                                                                                                                                                                 InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD_C.
InterPro; IPR006114; 6PGD_C.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR006184; 6PGdOm_BS.
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MEDLINE=95024018; PubMed=7937867;
Nelson K., Selander R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 177:1788-1796(1995)
                                                                                                                                                                                                                                                                                                                                                                        binding 2; 1.
                                                                                                                                                                                                                                                                                                                   6PGdom BS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VESLETPRRILLMYKAGAGTDSAIDSLKPYLDK------GDIIIDGGNTFFQDTI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VT-----YIGADGAGHYVKWVHNGIEYGDMQLIAEAYALLKGGLALSN--EELAQTFT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 DILNQGQLASIFLDQKCQNILQGNF-KPDFYLKYIQKDLRLAIALGDAVNHPT----
                    dehydrogenase gene (gnd) in enteric bacteria.";
Proc. Natl. Acad. Sci. U.S.A. 91:10227-10231(1994).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
    "Intergeneric transfer and recombination of the 6-phosphogluconate
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                                                                                                   PATHWAY: Hexose monophosphate shunt. Selongs to the 6-phosphogluconate dehydrogenase
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A INTERPROPER PROBBER PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PR
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421 V -> F (IN REF. 2).
51328 MW; FFIEBSE7665FDC90 CRC64;
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Last annotation update)
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ID 6PGD_SCHPO STANDARD;

AC P78812; Q9UQM5;

DT 15-JUL-1998 (Rel. 36, Created)

DT 16-OCT-2001 (Rel. 40, Last seq

DT 28-FEB-2003 (Rel. 41, Last ann
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RA WOOLNUE = LISBURGUE, FUDNED ELIB DE SUR M. Lyne M., Lyne R., Stewart A., RA WOOD V., GWILLIAM, R. Rajandream M.A., Lyne M., Lyne R., Stewart A., RA WOOD V., GWILLIAM, R. Rajandream M.A., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chilliamyorth T., Churcher C.M., RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., RA Holroyd S., Hornsby T., Howarth S., Murphy L., Niblett D., Odell C., RA Holroyd S., Moules M., Leather S., McDonald S., McLean J., RA Nooney P., Moule S., Munch M., Rabbinowitsch B., Althorit K., Paylor K., Rutter S., Saunders D., Seeger K., Sharp S., Retton J., Simmonds M., Squares R., Squares S., Stevens K., Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woolward J., Volckert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckert G., Aert R., Robben J., Grymonprez B., Wodward J., Langer II., Bager M., Schaefer M., Mueller-Aner S., Ra Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Galbert R., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Adlibert R., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Dominguez A., Revella J.L., Moreno S., Allada V.A., Garzon A., Thode G., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Three Somme sequence of Schizosaccharomyces pombe.";

RA Lute 415:871-880(2002).

C. - Physphate + CO(2) + Mapph.

RA Lute 415:871-880(2002).

C. - Physphate + Rodol Physph.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Voshioka S., Kato K., Nakai K., Okayama H., Nojima H.; "Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- PATHWAY: Hexose monophosphate shunt.
-i- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
InterPro; IPR006113; 6PGD_C.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_NaD.
InterPro; IPR006184; 6PGD_NaD.
InterPro; IPR006184; 6PGD_NaD.
InterPro; IPR006184; 6PGD_NaD.
IPEm; PP00393; 6PGD; 1.
PEm; PP033446; NaD binding_2; 1.
PRINTS; PR00076; 6PGDHRGNASE.
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PIR, T40628; T40628.
HSSP; P00349; 2PGD.
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                                                                                                                                                                                                                                 Schizosaccharomyces.
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                                                                                                                                                                                                    69 KKPRVCILLVKAGKPV----DYLIEGLAPLLEKGDIIVDGGNSHYPDTTRRCEELAKKGI 124
                                                                                                                                                                                                                             RFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTS-----FFLGEVGNA 433
                                                                                                                                                                                                                                             434 AKWMLIVNMVQGSFMATIAE-----GLTLAHVTGQSQQTLLDIL---NQGQLASIFLD 483
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                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=301 / Serotype 2a;
MEDLINE=2272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Zhang X., Zhang Y., Zhang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
6-phosphoglucomate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                          4.8%; Score 138.5; DB 1; Length 492; 22.9%; Pred. No. 0.16; Live 53; Mismatches 127; Indels 49
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MEDLINE=94131953; PubMed=7507920;
Morona R., Mavris M., Fallarino A., Manning P.A.;
"Characterization of the rfc region of Shigella flexneri.";
"J. Bacteriol. 176:733-747(1994).
                                                                                                                           271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPA-
         PROSITE; PS00461; 6FGD; 1.
Oxidoreductase; Pentose shunt; NADP.
CONFLICT 219 220 IA -> ST (IN REF. 1).
SEQUENCE 492 AA; 53679 MW; F55F342957A9D3E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           468 AA
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MEDLINE=22590274; PubMed=12704152;
TIGRFAMS; TIGR00873; gnd; 1.
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                                                                                                   68; Conservative
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                                                                                      Local Similarity
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P37756;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                     SEQUENCE OF 12-456 FROM N.A.
STRAIN=ATCC 29903,
MEDLINE=95024018; bubMed=7937867;
MEDLINE=95024018; bubMed=7937867;
Melson K., Selander R.K.;
"Intergeneric transfer and recombination of the 6-phosphogluconate dehydrogenase gene (gnd) in enteric bacteria.";
Proc. Natl. Acad. Sci. U.S.A. 91:10227-10231(1994).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulos
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                       -1- PATHWAY: Hexose monophosphate shunt.
-1- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
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l Similarity 20.7%; Pred. No. 0.18;
68; Conservative 54; Mismatches 100; Indels 106;
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Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 AA; 51344 MW; 2203A0D82120CD61 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006114; 6PGD C.
InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR006184; 6PGdom BS.
Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDKGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE015225; AAN43630.1; -. AE016985; AAP17458.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U14468; AAC43834.1; -.
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Best Local Similarity
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D90841; BAA15869.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88086897; PubMed=3275621;
Barcak G.J., Wolf R.E. Jr.;
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"Comparative nucleotide sequence analysis of growth-rate-regulated "Comparative nucleotide sequence of Escherichia coli and from Salmonella typhimurium LT-2.";
J. Barceriol. 170:372-379 (1988).
-i. CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                       SIRAIN=K12 / MG1655;
MEDLINE=97426617; bubMed=9278503;
MEDLINE=97426617; bubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89126937; PubMed=2464736;
Miller R.D., Dykhuizen D.E., Hartl D.L.;
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the 6-phosphogluconate dehydrogenase gene in Escherichia coli.";
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                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
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Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
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corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
              6PGD_ECOLI STANDARD; PRT; 468 AA.
P00350; P78080;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 31, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
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Science 277:1453-1474(1997).
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"DNA sequence of the Bscherichia coli gene, gnd, for G-phosphogluconate dehydrogenase.";
Gene 27:253-264(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Hexose monophosphate shunt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-125 FROM N.A. MEDLINE=89126937; PubMed=2464736;
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EMBL; AE000294; AAC75090.1; -.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                              Escherichia coli.
                                                                                                                                         GND OR B2029.
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6PGD ECOLI
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LETPRRILLMVKAGAGTDAAİDSLKPYLDK-------GDIIIDGGNTFF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 ODTIRRNRELSAEGFNFIGTGVSGGEEGALKGPSIMPGGQKEAYELVAPILTKIAAVAED 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 CSSCFQAMGKTSFFLGEVGNAAKWMLIVNNWVQGSFMATIAEGLTL----AHVTGQSQQTL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 FTEWNNGELSSYLIDITKDIFTKKDED---GNYLVD-------VILDEAANKGT 262
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                                                                                                                                                                                                                                                                                                                                                                                                                4.7%; Score 136; DB 1; Length 468;
0.0%; Pred. No. 0.21;
ve 54; Mismatches 106; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                               Pfam; PF00393; 6PGD; 1. Pfam; PF00393; 6PGD; 1. Pfam; PF03446; NAD binding 2; 1. Transmars, Pro0076; 6PGDHDRGNÄSE. TIGREAM; TIGROR973; 9MG; 1. PROSITE; PS00461; 6PGD; 1. Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                            306 306 P -> R (IN REF. 1).
468 AA; 51481 MW; 62A32C84DC596D86 CRC64;
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 EAPVSGNQQLSNDGMLVI---LAAGDRG---
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                                                                                                                                                                              InterPro; IPR006114; 6FGD_C.
InterPro; PR0066113; 6FGD_decarbox.
InterPro; IPR0066115; 6FGD NAD.
InterPro; IPR006184; 6FGGOm_BS.
                                                                                                                                             InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                HSSP; P00349; 2PGD.
ECO2DBASE; C042.6; 6TH EDITION.
EcoGene; EG10411; gnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                 20.08;
               M23181; AAA23924.1;
M18956; AAA23919.1;
M18957; AAA23920.1;
M18960; AAA23922.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Conservative
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                                                                                 D64968; DEECGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
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                                                               EMBL;
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EMBL; AE003763; AAF56762.2; -. EMBL; AY118404; AAM48433.1; ALT_FRAME.

R Flybase; FBgn003959; Mes-4.

R GO; GO:000228; C:nuclear chromosome; ISS.

GO; GO:000228; C:nuclear chromosome; ISS.

GO; GO:00454; F:histone methyltransferase activity; ISS.

GO; GO:001892; P:gene silencing; ISS.

R GO; GO:001892; P:gene silencing; ISS.

R InterPro; IPR003616; PostSET.

R InterPro; IPR00313; PWWP Gomain.

R InterPro; IPR001214; SET.

R InterPro; IPR001265; Znf PHD.

R Pfam; PF00656; SET; 1.

R Pfam; PF00656; SET; 1.

R SMART; SM00579; PWWP; 1.

R SMART; SM00249; PHD; 3.

R SMART; SM00129; PWWP; 2.

R SMART; SM00129; PWWP; 2.

R PROSITE; PS50868; DSST; 1.

R PROSITE; PS50818; PWWP; 2.

R PROSITE; PS50818; PWWP; 2.

R PROSITE; PS50818; ZE PHD 1; 1.

R PROSITE; PS501159; ZE PHD 1; 1.

R PROSITE; PS501159; ZE PHD 2; 1.

R PROSITE; PS501159; ZE PHD 2; 1.

R PROSITE; PS501159; ZE PHD 2; 1.

R PROSITE; PS50115; ZE PHD 2; 1.

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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Bruton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Bratton G.G., Wortman J.R., Mandews P.E., Champe M., Ffeiffer B.D.,

Am K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Ballew R.M., Basu A., Baxndale J., Bayraktaroglu L., Beasley E.M.,

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Ballew R.M., Basu A., Burder B.P., Bhandari D., Boldhakov S.,

Barkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier S.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawleys J., Dhlke C., Davenport L.B., Davies P., Chandra I.,

Cherry J.M., Cawleys S., Dahlke C., Pavenport L.B., Davies P., Chandra I.,

B. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plaischmann W.,

R.A. Boodson K., Doup L.E., Downes M., S., Gelbart W.M., Glasser K.,

B. Doubin K.J., Barvey D.A., Hemann T.J., Hernandez J.R., Houck J.,

B. Hostin D., Houtson K.A., Howland T.J., Wei M.-H., In Early M.,

B. Hostin D., Houtson K.A., Howland T.J., Hernandez J.R., Houck J.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

B. Alalish P., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasco P., Lei Y., Levitisky A.A., Li J.H., Li Z., Liang Y., Lin X.,

Mattei B., Mointosh W., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Woly M., Murphy B., Murphy I., Muzny D.M., Nelson H.,

R. Alenert K., Remingor K., Stunders R.D. C., Scheeler F., Shen H.,

Spirskas R., Tector C., Turner R., Venice E., Wang A.H., Wang X.,

Mulliams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Zhon C.,

Shen Bronner R., Morley R., Rohlistock G., Wu D., Yang S., Zhon C.,

Shen Bronner R., Morley R., Rohlistock S., Shith T.,

Albers R., Morris G., Wolley K.C., Wu D., Yang S., Zhon S.,

Shishor R., Morley R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000).
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STRAIN-Berkeley; TISSUE-Embryo;
STRAIN-Berkeley; TISSUE-Embryo;
STRAIN-Berkeley; TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J.M., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.E.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Potential histone methyltransferase. Histone methylation
gives specific tags for epigenetic transcriptional activation or
repression (By similarity).
-! SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 3 PHD-type zinc fingers.
-!- SIMILARITY: Contains 1 post-SET domain.
-!- SIMILARITY: Contains 2 PwWP domains.
-!- SIMILARITY: Contains 1 SET domain.
-!- SIMILARITY: Contains 1 SET domain.
-!- CAUTION: Ref. 3 sequence differs from that shown due to a
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frameshift in position 348.

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                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                      1109 IEGDIGDGHK-----TKSQLFRNYTIGVERASRFLPIIKARRQEQDMERQSGN 1156
                                                                                                                                                                                                                                                                                                                                                         64 -----HAHKEEMIKINKGKRFQQAVDAVEEFLR-----RAKGKDQTSSHNSSD 106
                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                ch 4.7%; Score 135.5; DB 1; Length 1427; l Similarity 30.7%; Pred. No. 0.98; 35; Conservative 16; Mismatches 40; Indels 23;
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POLY-GLY.
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Best Local
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PWWP 1 PHD-TYPE 1. PHD-TYPE 2. PHD-TYPE 3.

468

DOMAIN ZN_FING ZN_FING ZN_FING DOMAIN

DOMAIN DOMAIN

POST-SET PWWP 2. SET

Search completed: September 16, 2004, 07:30:47 Job time: 17 secs

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X Mawi J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Kawai J., Shinagawa A., Shibata K., Xoshino M., Itoh M., Ishii Y., Xawai J., Shinagawa A., Shibata K., Xoshino M., Itoh M., Ishii Y., Xawaa J., Saho T., Okazaki Y., Golobori T., Bono H., Xasukawa T., Saito R., Saito T., Okazaki Y., Golobori T., Bono H., Xasukawa T., Saito R., Saito T., Casai C., King B., Kochiwa H., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Raki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Riingwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanghian H., Weltz C., Whittaker C., Wilming L., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR000637; AT_hook.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 ICBEBIGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKCDLFIQEGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPWAAAANEVYKRAKALDQS
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 EK-----EGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLLDIINQGQLASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                7;
                                                                                                                                               DB 11; Length 546;
                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003693; AAH03693.1; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                         B3AC1562477ABC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last annotation updated Similar to RIKEN cDNA 3930401K13 gene (Fragment) Homo sapiens (Human).
                                                                                                                                           95.8%; Score 2745.5; DB 96.6%; Pred. No. 2e-184; iive 8; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523
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InterPro; IPR000313; PWWP_domain. Pfam; PF002178; AT hook; 1. Pfam; PF03446; NND binding_2; 1. Pfam; PF00855; PWWP; 1.
                                                                                                        546 AA; 59744 MW;
                                                                    SMART; SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
SEQUENCE 546 AA; 59744 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNDMSAVYRAYIH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNDMSAVYRAYIH 546
                                                                                                                                                                           Matches 534; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                            Best Local Similarity
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FlyBase
  1;
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                                                                                                                                                                                                                                                                                                                                                                                                      373
                                                                                                                                                                                                                                                                                                                                                                                                                   433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 VIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553
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                                                                                                                                                                                                                                                                                                                                                              ADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLF1QEGARL 313
                                                                                                                                                                                            73
                                                                                                                                                                                                              9
   . .; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKPDFYLKYIQKDLRLAIALGDAVNHPTPWAAAANEVYKRAKALDQSDNDMSAVYRAYIH
                                                                                                                                                                                                                                  74 NKGKRFQQAVDAVBEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDEKRKLSLSE
                                                                                                                                                                                                                                                                                               121 GKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTIPESSTVKGMM
                                                                                                                                                                                                                                                                                                                     AGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICEBETGSTSIQA
                                                                                                                                                                                                                                                                                                                                                                          GRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                VIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKNMLIVNMVQGSFMATIAEGLTLAQVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAYIH
                                                                                                                                                                                                                                                                            GKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDBKDLTIPESSTVKGMM
                                                                                                                                                                                                                                                                                                                                          ---ETGSTSIOA
                                                                                                                                                                                           14 GKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAHKEEMIKI
                                                                                                                                                                                                            1 ĠĸĹĠĸŶ₽PwPĠĸĮVNPPKDĽKKPRĠĸĸĊFFVKFFĠTEDHAWIKVEĢĹKPYHAHKEEMIKI
                                                                                                                                                                      17; Gaps
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla... GO; GO:0006098; P:pentose-phosphate shunt; IEA. GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. InterPro; IPR006115; GFGD NAD. InterPro; IPR00613; AT hook. InterPro; IPR00013; WWP-domain. Pfam; PF02178; AT hook; 1. Pfam; PF02178; AT hook; 1. Pfam; PF03146; NAD binding_2; 1. Pfam; PF03446; NAD binding_2; 1. SMART; SM00885; PWF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                  4; Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
                                                                                                                                                                                                                                                                                                                                         181 AGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEK-------
                                                                                                                                                                       Indels
                                                                                                                             ED3E2853938A211F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8T079; Q9VL51;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
LD22344p (CG4747-PA).
BEST:LD227483 OR BEST:LD29743 OR CG4747.
                                                                                                                                               Score 2683.5; DB 4
Pred. No. 4.2e-180;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 AA
                                                                                                                              57215 MW;
                                                                                                                                                  93.6%;
                                                                                                                                                              Best Local Similarity 96.7
Matches 522; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                523 AA;
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                                                                                                                                SEQUENCE
                                                                                                                                                     Query Match
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Connade W. Chave C., Doreate V., Fariba D., Fries E., George R., Gonnade W. Chave C., Doreate V., Fariba C., Miranda A., Mungall C.J.

R. Gonnade W. Chave C., Doreate V., Fariba S. Phonamenavong S., Wan K., W. C., Leaks S. E., Rubhi G.M., Colniker S., Phonamenavong S., Wan K., W. C., Leaks S. E., Rubhi G.M., Colniker S., Phonamenavong S., Wan K., W. C., Leaks S. E., Rubhi G.M., Colniker S., Abbarre M. M., Golden S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., Mandreon S., M
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Pred. No. 5e-43;
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                                                                                                                                                                                                                                                                                                                                           PFam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
        [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                     TISSUE=Panicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
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Q94B07;
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                                                                                                                                                                                                                                                                                                                                                                                     126 KRKLSLSEGKVKKNMGEGKKRVSSGSSERG-----SKSPL-----KRAQEQS 167
                                                                                                                                                                                                                                                                                                                                                                                                                    SEBIVGEEATADGNNGVVAHVV--GSPDEGDGLDVEINADSSASPVTSPAVTTKAAGKRT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KRGRPPKDEKDLTIPESSTVKGMMAGPMAAFKWQPTAS-EPVKDADP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 ASSTPTGRRRVETDALLASIAAKRAPNAIALLDRPVVTRPEAQVIDMSSRSNTLADRDIV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DITFACVSDPKAAKDLVLGPSGVLQGIRP--GKCYVDMSTVDADTVTELAQVIVSRGGRF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNM 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILGVSLVGLAEALALADRFSISLNDIIDIFDLTSMKSPMLLAKGKEMAKGDFNPQQPLSH 551
                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                            66 HKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                  DLVWGKLGRYPPWPGKIVNPPKDL - - - KKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 VQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cooper B., Hutchison D., Park S., Guimil S., Luginbuhl P., Ellero C., Goff S., Glazebrook J.;
"Identification of Rice (Oryza sativa) Proteins Linked to the Cyclin-Mediated Regulation of the Cell Cycle.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Epperatophyta, Nagnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Gamma hydroxybutyrate dehydrogenase-like protein (Hypothetical
                                                                                                                                  DB 5; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 IQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                      602 AA; 65252 MW; E004EEC610C23625 CRC64;
                                                                                                                              Query Match 27.8%; Score 796.5; DB 5; Best Local Similarity 32.8%; Pred. No. 1.8e-47; Matches 192; Conservative 110; Mismatches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 AA.
    Pfam; PF03446; NAD_binding_2;
                                          SMART; SM00293; PWWP; 1.
PROSITE; PS50812; PWWP; 1.
SEQUENCE 602 AA; 65252 N
Pfam; PF00855; PWWP; 1.
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SEQUENCE FROM N.A
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 24, Last amontation update)
6amma hydroxybutyrate debydrogenase (EC 1.1.161).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                    :
                                                                                                                                                  EMBL, AB110167; BAC78559.1; -.
GO; GO:0008442; F:3-hydroxytaeobutyrate dehydrogenase activity; IEA.
GO; GO:00004616; F:phosphogluconate dehydrogenase (decarboxyla. ..;
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
InterPro; IPR00204; 3hydroxisobut_dh.
InterPro; IPR006183; GPGD_NAD.
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"Plant gamma-hydroxybutyrate dehydrogenase, a novel fermentation enzyme.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. - SEQUENCE 293 AA; 30496 MW; 2362B7AC4EE52038 CRC64;
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SEQUENCE FROM N.A.
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           Query Match
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                                                                                                                                                                                                                           AMLSDPCAALSVVFDKGGVLEQICEGKGYIDMSTVDAETSLKINEAITGKGGRFVEGFVS 121
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EMBL; AB025639; BAB01322.1; -.

GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO; GO:0006461; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.

GO; GO:0006098; P:pentose-phosphate shunt; IEA.

GO; GO:0006573; P:valine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                      Dehydrogenase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                Gaps
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                                                                                                        24.3%; Score 697; DB 10; Length 289; 49.6%; Pred. No. 6.2e-41;
                                                                                                                               Indels
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SEQUENCE 289 AA; 30691 MW; 3E67002A19706636 CRC64;
                                                                                 289 AA; 30678 MW; 3E6715DFF96593D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                            242 LALALGDENAVSMPVAAAANEAFKKARSLGLGDLDFSAVIEA
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                93;
                                                                                                                                49; Mismatches
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Interpro; IPR006183; 6FGD.
Interpro; IPR006118; 6FGD NAD.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
           InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
PROSITE; PS00895; 3_HYDROXXISOBUT_DH;
Oxidoreductase.
InterPro; IPR002204; 3hydroxisobut_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE-20277480; PubMed-10819329;
                                                                                                                                Matches 140; Conservative
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                                                                                                                    Local Similarity
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                                                                                    SEQUENCE
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                                                                                                                                                              EVGFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVEHGASVCESPAEVIKKCKYTI
                                                                                                                                                                                                                                                                                                                                                                                     GNOOLSNDGMLVILAAGDRGLYEDCSSCFOAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
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SOUTHWICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
   Length 289;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
24.2%; Score 695; DB 10;
49.6%; Pred. No. 8.6e-41;
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                                 ; Pred. No. 8.6¢ 49; Mismatches
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                  Matches 140; Conservative
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Genome Biol. 0:0-0(2002).
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                                    Best Local Similarity
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Similarity
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                                                                                                                                                                        PRIPLRFRPKPISP-----FL---SKPQICLAYRVYSSLQSTTPSTRDELGTVS
                                                                                                                                                                                                  251 IQAADSTAVNGSITPIDKKIGFLGLGLMGSGIVSNLLKMGHIVIVWNRTAEKCDLFIQEG
                                                                                                                                                                                                                        -----IGFLGMGIMGSPMAQNLIKAGCDVTVWNRTKSKCDPLVGLG
                                                                                                                                                                                                                                                                                            371 LAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEV
                                                                                                                                                    PMAAFKWOPTASEPVKDADPHFHHFLLSQTEKPAVC----YQAITKKLKICEEETGSTS
                                                                                                                                                                                                                                                                                                                                                                                     491 GGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE S., Buehler B., Chao Q., Johnson-Hopson C., Kim C., Khan S., Brooks S., Buehler B., Chin C., Chiou J., Choi B., Conn L., Chin P., Altali H., Bei Q., Chin C., Chiou J., Choi B., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Lenz C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Sperimtophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
EMBL; AY085690; AAM62909.1; -.
EMBL; BT008734; AAP42747.1; -.
GO; GO:0004616; F:phosphorate dehydrogenase (decarboxyla...)
GO; GO:0006098; P:pencose-phosphate shunt; IEA.
InterPro; IPR006115; GPGD NAD.
Pfam; PF03446; NAD binding_2; 1.
Hypothetical protein.
SEQUENCE 343 AA; 36287 NW; D012C16284C5FA52 CRC64;
                                                                                                                               38;
                                                                                                        Length 343;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .-OCT-2000 (TrEMBLrel. 15, Last sequence update)
                                                                                                                               64; Mismatches 116;
                                                                                                       23.3%; Score 667; DB 10; 39.4%; Pred. No. 1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Submitted (FEB-2000)
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Submitted (APR-2000)
                                                                                                                  Similarity
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                                                                                                                          Matches 142;
                                                                                                       Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lerz C., Li, J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Submitted (UN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC022492; AAF79475.1; -...
EMBL, Schoudsdis, Piphosphogluconate dehydrogenase (decarboxyla., IEM GO; GO:0006698; P:pentose-phosphate shunt; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 SSSSKAMALCSICPRIPLRFRPKPISP-----FL---SKPQICLAYRVYSSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 KLKICEEFTGSTSIQAADSTAVNGSITPIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IGFLGMGIMGSPMAQNLIKAGCDVTVWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 ATIABGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --DLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Arga5530/WML2 15.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.5%; Score 644; DB 10; Length 387; 36.3%; Pred. No. 5e-37; ive 65; Mismatches 121; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 SSTVKGM----MAGPMAAFKWQPTASEPVKDADPHFHHFULSQTEKPAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arabidopsis cDNA clones.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 RTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                    0445432CE8CA0137 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03446; NAD_binding_2; 1.
SEQUENCE 387 AA; 41484 MW; C
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 146; Conservative
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Local Similarity
es 90, Conserv
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SEQUENCE 300 AA;
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22
                                       112
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                                                                                                                                                                            269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                 GNQQLSNDGMLVILAAGDRGLXBDCSSCRQAMGKTSFFLGEVGNAAKAMLIVNMVQGSFM 448
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                                                                                                                                                                                                                    329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                              2 EVGFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVEHGASVCESPAEVIKKCKYTI
                                                                                                                                                         Gaps
       GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla...;
GO; GO:0006039; P:pentose-phosphate shunt; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR00213; GPGD.
InterPro; IPR006115; GPGD.NAD.
InterPro; IPR006115; GPGD.NAD.
InterPro; IPR03446; NAD.binding_2; I.
PRINTS; PR0346; NAD.binding_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%; Score 560; DB 10; Length 343; 40.5%; Pred. No. 3.3e-31; ive 49; Mismatches 83; Indels 5:
                                                                                                                                     Length 248;
                                                                                                                                                      66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone:B1151A10.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003413; BAB91904.1; -.
                                                                                                      PROSITE, PS00895; 3 HYDROXYISOBUT DH; 1.
SEQUENCE 248 AA; 26336 MW; C96912B3E2A7E677 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                    19.6%; Score 562; DB 10;
51.7%; Pred. No. 1.5e-31;
iive 36; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                             Putative gamma hydroxybutyrate dehydrogenase.
                                                                                                                                                                                                                                                                                                     449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLAS 479
                                                                                                                                                                                                                                                                                                                 182 NAFSEGLVLADKSGLSSDTLLDILDLGAMTN 212
                                                                                                                                                                                                                                                                                                                                                                            343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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                                                                                                                                                          Matches 109; Conservative
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Sasaki T., Matsumoto T.
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                                                                                                                                                Local Similarity
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Best Local 9
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                                                                                                                                      Query Match
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Matches
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PEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN-C2A / AICC 35395 / DSM 2834;

STAIN-C2A / AICC 35395 / DSM 2834;

STAIN-C2A / AICC 35395 / DSM 2834;

SALAN-C2A / AICC 35395 / DSM 2834;

A STAIN-CA / AICC 35395 / DSM 2838;

A Allan N., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allan N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Epinger T.A., Umayam L.A., White O., White R.H., de Macario B.C., Prichett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., McTchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., McTchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Amphysiological diversity., "The genome of Methanosacina acetivorans reveals extensive metabolic R. The Golome Res. 12:522-542(2002).

REMBL, AEOINZ2; AAM04058 H. ..

ROJ GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. ..; IEA.)

ROJ GO:0006098; Pipencoe-Phosphate shunt; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 DITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326
                                                                                                                                        AMLADPESAVEVACGANGAAQGMAPGKGYVDVSTVDAATSKLIGKHITSTGASFLERC-- 169
                                                                                                                                                                                                                 424
                                                                                                                                                                                                                                                                                         -----DFSSCTVGPMLTRYLFSRLQFQAQKSQQKMGCSSFLP 206
                                                                                                                                                                                                                                                                                                                                                             425 ---FFLGEVGNAAKMMLIVNNVQGSFMATIAEGLTLAHVTGOSQQTLLDILNQGQLASIF 481
                                                                                                                                                                                                                                                                                                                                                                                                                  207 QSRFFLGDVGKGADMKLVVNMVMGSMMVSFSEGLLLSEKVGLDPNTLVEVISQGAISAPM 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKNITVGVIGLGIMGSSFASNLLSRGYNVHVYNRTKEKAQPLIERGATFHSTPRELASVA 66
KVGFLGLGIMGAPMASNLINAGCDVTVWNRTRSKCDPLLSLGAKYEPSPADVASSCDVTF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 FSLKGPSMVKAAYPTAFPLKHQQKDLRLALALALALAESVSQSIPTVAAANELYKVAKSLGLAD
                                                                        329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                        -----FQA-----MGKTS---
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Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
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ilarity 31.8%; Pred. No. 7.8e-20;
Conservative 47; Mismatches 144;
                                                                                                                                                                                                                        389 GNQQLSNDGMLVILAAGDRGLYEDCSSC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD_binding_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanosarcina acetivorans.
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Sulfolobus.
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Best Local S
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Matches
                                                                                                               RESULT 15
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385 APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQ 444
                                                                                                                                                                                 GSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQ 504
                                                                                                                                                                                                                                                                                                                                                          | ::| | :: | | :: | | :: | | :: | | :: | | | :: | | | :: | | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | | :: | | :: | | :: | | | :: | | | :: | | :: | | | | :: | | :: | | :: | | :: | | | :: | | :: | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
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PIR; C70303; C70303.
G0; G0:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
G0; G0:0006098; F:pentose-phosphate shunt; IEA.
InterPro; IPR008927; 6DGDH C. like.
InterPro; IPR006183; 6PGD. C. like.
InterPro; IPR00611S; 6PGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C. PEGD. C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 KDLKLVNEQITKTGAILPMTKVSIREYSRTVQNGEGQKDFSVI 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 AA; 31788 MW; 60E79AF4954D4294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
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Best Local Similarity
Matches 90; Conserv
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SEOUENCE 288 AA:
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Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                     445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRRLEAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 VSVVEGLLLARSLGIDDDKLFSVLSTGAANSFTVQYYLPKIMKGDLNPGFKAAHLKKDLK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0008412; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
GO; GO:0006038; P:pentose-phosphate shunt; IEA.
InterPro; IPR00519; P:pantose-phosphate shunt; IEA.
InterPro; IPR00519; GPGD.
InterPro; IPR00518; GPGD.
InterPro; IPR00518; GPGD.
InterPro; IPR00518; GPGD.
InterPro; IPR00519; GPGD.
InterPro; IPR00519; GPGD.
InterPro; IPR00519; GPGD.
InterPro; IPR00504; RNA. rec_mct.
Ffam; PF03446; NAD binding 2; I.
PRINTS; PR0076; GFGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 35092 / DSW 1617 / P2;
STRAIN-ATCC 35092 / DSW 1617 / P2;
STRAIN-ATCC 35092 / DSW 1617 / P2;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moores A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duquet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSO1560.
Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 LAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 AA; 31025 MW; 4EEA33390300E7C7 CRC64;
                                                                                          Last sequence update)
Last annotation update)
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29.3%; Pred. No. 1.7e-19;
tive 68; Mismatches 132;
289 AA
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PROSITE; PS00030; RRM_RNP_1; 1.
                                                             Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE006770; AAK41774.1; -. PIR; G90314; G90314.
                                                   01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
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PRELIMINARY;
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2;

5,

Indels

48; Mismatches 152;

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Conservative
96;
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                                                                                                                                                                                                                                                                                                                                                                                                  203
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Q97DX8
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Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Yamada K., Banh J., Banno F., Chang E., Dale J.M., Wu H.C.,
Yamada X., You G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
Yamamura Y., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Kim C., Koesema E., Lum B., Lini J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.; Dan of gene AT4g29120 (GI:7269810).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AL161574; CAB79670.1; -.

EMBL, AL161574; CAB79670.1; -.

EMBL, AN062952; AAL33784.1; -.

EMBL, AN062952; AAL33784.1; -.

EMBL, AR3704041; F.oxidoreductase activity; IEA.
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinn zaki K., Davis R.W., Ecker J.R., Theologis A.; Full Length cDNA of gene AT4929120 (G1:7269810).";
                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicocyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                          Last annotation update)
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Pred. No. 7.4e-19;
                                                                                     Last sequence update)
                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last annotation ul
Hypothetical protein (Putative dehydrogenase)
F19B15.150 OR AT4G29120.
            334 AA
                                                              Created)
            PRT;
                                                                                     (TrEMBLrel. 13,
            PRELIMINARY;
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334 AA; 3
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01-MAY-2000
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13.4%; 32.2%;

Query Match Best Local Similarity

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254 ADSTAVNGSITPIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARL 313
                                                                                                                                                                                              314 GRIPAEVVSTCDITFACVSDPKAAKDLVLGP-SGVLQGIRPGKCYVDMSTVDADIVTELA 372
                                                                                                                                                                                                                                                          84 ADSPNSVAEQSDVVFTIVGYPSDVRHVLLDPKSGALSGLRGGRGVUDWITSEPSLAEEIA 143
                                                                                                                                                                                                                                                                                                                                                                                            QVIVSRGGRFLBAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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                                                            24 ASSTISSDIITPSNTKIGWIGTGVWGRSMCGHLIKAGYTVTVFNRTISKAQTLIDWGANV
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MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acecobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
BIR, S97310; G97310;
G9730; G97300; Priposphogluconate dehydrogenase (decarboxyla...;
GO: G0:0006098; P:pentose-phosphate shunt; IEA.
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InterPro; IPR006115; 6PGD_NAD.
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30.0%;
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Best Local Similarity
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STRAIN-USDA 110;
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BLR6094.
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Q89HA0;
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127 GGDIGAAEGTLSIMVGGDKEAFDALMPIFELMGKNIVLQGSAGSGQHTKMCNQIAIASNI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).

EMBL, AE008066; AAL63233.1; -.

GO; GO:0008422; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO; GO:000615; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.

GO; GO:0006573; P:valine metabolism; IEA.

InterPro; IPR0051204; 3hydroxisobut_dh.

InterPro; IPR005115; GFGD_NAD.

InterPro; IPR006115; GFGD_NAD.

PRINTS; PR00076; GFGBHDRGNASE.
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.0%; Score 373; DB 17; Length 284; Best Local Similarity 30.2%; Pred. No. 3.5e-18; Matches 80; Conservative 54; Mismatches 131; Indels (
                                                                                          LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
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Hypothetical protein; Complete proteome.
SEQUENCE 284 AA; 30155 MW; 9D845881717D8550 CRC64;
                                                                                                                                                                                                                                                   Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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PAE1145.
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NCBI_TaxID=13773;
                                                                                                                                                                PRELIMINARY;
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01-MAR-2002 (
01-JUN-2003 (
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RESULT 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genomic sequence of nitrogen-fixing symbiotic bacterium landyrhizoblum japonicum USDA110.";

BNB 19 189-197 (2002).

EMBL; AP005957; BAC51359.1; -..

EMBL; AP005957; BAC51359.1; -..

EMBL; AP005957; PR06159; Priphosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO; GO:0006408; P:pencose-phosphate shunt; IEA.

InterPro; IPR06115; 6FGD.

PITCEPPO; IPR06115; 6FGD NAD.

PEM PF03446; NAD binding 2: 1.

PRINTS; PR00076; 6FGDHDRGNASE.
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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                                                                     Last sequence update)
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PRT;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:penctose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
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                                                                  .; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C., Read T.D., Bisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Despon A., Scott J. Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Hatt D.H., Kolonay J.F., Madupu R.T., Weidman J., Umpraim M., Lee K., Berry K., Dee C., Wanathevan J., Weidman J., Impraim M., Lee K., Rerry K., Dee C., Feldblyom T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Feldblyom T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG
                                                                                                                                                                                                                                                                                                                                     390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                 Gaps
STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010190; AAL80840.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla.GO; GO:0006089; P:pentose-phosphate shunt; IEA.
InterPro; IPR008927; 6DGDH C_like.
InterPro; IPR006115; 6PGD_NAD.
                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                          DB 17; Length 278;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AYDLAVASRKAVPLNATVREIYRLAFEKGLEELDFSVVYRLF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                          AIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                               D755E046098D93B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-hydroxy-3-oxopropionate reductase.
                                                                                                                                                                                     ; Pred. No. 6.5e-18; 50; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AA
                                                                                                                                                                           12.9%; Score 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015716; AAN55796.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                 278 AA; 31376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                       32.3%;
                                                                                                                                                                                                    91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shewanella oneidensis.
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                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                   Complete proteome SEQUENCE 278 AA
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FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLBAPV 387
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MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Rurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                      269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE-GARLGRTPAEVVSTCDIT
                                                                                                                                                                                                                                                                                                                                            FTCVGNDNDLREVVLGDDGVIHGMALGTVLVDHTTASADVARELHKVLGEKGIDFLDAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVN-----
                                                                                                                                                                                                                                                    Gaps
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EMBL; AP002564; BAB37426.1; -.
PIR; C85974; C85974.
PIR; C9129; C91129.
PIR; JQ0613; JQ0613.
GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=21074995; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                     DB 16; Length 291;
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                                                                                                                          31510 MW; 7B7CD7FCA9DB29DB CRC64;
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Last annotation update)
                                                                                                                                                                                     12.9%; Score 368.5; DB 16; 30.4%; Pred. No. 7.5e-18; iive 64; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299
InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD binding 2; 1.
PROSITE: P800895; 3 HYDROXYISOBUT DH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 20, TrEMBLrel. 20, (TrEMBLrel. 24,
                                                                                                                                                                                     Ouery Match
Best Local Similarity 30.4*
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:529-533(2001).
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01-JUN-2003 (TrEMBLrel.
Putative dehydrogenase.
                                                                                                                                   291 AA;
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                                                                                              Complete proteome. SEQUENCE 291 AA;
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269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 TMLPNSPHVKEVALGENGIIEGAKPGTVLIDMSSIAPLASREISDALKAKGVEMLDAPVS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 ATIAEGLTLAHVTGQSQQTLLDDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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Nature 423:89-91(2003).

BMBL; AB017011; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO; GO:0008421; F:3-hydroxyisobutyrate activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.

GO; GO:0006098; P:pentose-phosphate shunt; IEA.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=22608415; PubMed=12721630;
MEDLINE=22608415; PubMed=12721630;
Kapatral V., Sorcin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Sonza M., Walunas T.,
Chu L., Mazur M., Goltsman E., Forstein N., D'Sonza M., Walunas T.,
Overbeek R., Kyrpides N.,
Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                               12.7%; Score 365; DB 16; Length 296; 28.7%; Pred. No. 1.3e-17; tive 59; Mismatches 140; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                   InterPro; IPR006398; TartTo sem_red.
Pfam; PP03446; NAD_binding_2; 1.
PRINTS; PR00076; GEDHDRGMASE.
TIGRFAMS; TIGR01505; tartro sem_red; 1.
PROSITE; PS000895; 3 HYDROXXISOBUT DH; 1.
Oxidoreductase; Complete protecome.
SEQUENCE 296 AA; 30728 MW; A62B62F3B91F9DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31987 MW; 8B04FC5E59A93423 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 NALDTSHGVGAQLPLTAAVMEMMQALRADGHGNDDHSAL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31).
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tive 63; Mismatches 144;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-CCT-2003 (TrEMBLrel. 25, Last ann
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InterPro; IPRO06115; 6PGD NAD.
Pfam; PPO3446; NAD binding 2; 1.
PRINTS; PRO0076; 6PGDHDRGNASE.
                 InterPro; IPR006115; 6PGD_NAD
                                                                                                                                                                                                                                                                                  Conservative
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Matches 76; Conservative
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                                                                                                                                                                                                                                                      Local Similarity
nes 80; Conserv
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                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNQQLSNDGMLV1LAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE008849; AAL22120.1; -. GO; GO: 0008679; F:2-hydroxy-3-oxopropionate reductase activity; IEA. GO; GO: 0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA. GO; GO: 00016491; F:: Aridoreductase activity; IEA. GO; GO: 0004616; F: phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO; GO: 0006098; P: pentose-phosphate shunt; IEA. GO; GO: 0006573; P: valine metabolism; IEA. INTERPRO; IRR002204; Bhydroxisobut_dh. IEA. InterPro; IRR006183; 6FGD.
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STRAINSIZ / GSGC112 / ATCC 700720;
STRAINSIZ / GSGC112 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MCC16-liand M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Waren E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                     2;
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla., GO:0006098; P:pentose-phosphate shunt; IEA., GO; GO:0006098; P:pentose-phosphate shunt; IEA. InterPro; IPR012204; Jhydroxisobut_dh.
InterPro; IPR06113; GFGD. NAD.
InterPro; IPR066115; GFGD. NAD.
InterPro; IPR066115; GFGD. NAD.
Fram: PF03446; NAD. Bhiding 2; 1.
PRINTS; PR00076; GFGDHDRGNASE.
TIGRPAMS; TIGR01505; tartro_sem_red; 1.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                              12.8%; Score 367; DB 16; Length 299; 29.4%; Pred. No. 9.9e-18; ive 57; Mismatches 140; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 LAIALGDAVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: | | : | | : | | 247 NALDTSHGVGAQLPITAAVMEMMQALRADGLGTADHSALACY 288
                                                                                                                                                                                                                                                                                                 299 AA; 31019 MW; 08E65F785BC2B566 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Tartronate semialdehyde reductase (TSAR) (EC 1.11.60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 AA
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Salmonella typhimurium.
                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 299 AA;
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RESULT 23 Q8ZLV8

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PS00895; 3_HYDROXYISOBUT_DH; 1.
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PROSITE;
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                                                                                                                      390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA 449
                                                                                                                                                                                450 TIAEGLILAHVIGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRL 509
 270 IGFLGLGLMGSGIVSNILKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
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SPRAIR-TY2 / ATCC 700931;
STRAIR-TY2 / ATCC 700931;
MEDLINE=22231367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                    8 IGFIGIGVMGKSMVYHIMQDGHKVYVYNRTKAKTDSLVQDGANWCNTPKELVKQVDIVMT
                                                                                                                                         : | : | : | : | | | | : | | | : | | | 1188 GVCEAVAYAKKAGLNPDKVLESISTGAAGSWSLSNLAPRMLKGDFEPGFYVKHFMKDMKI
                                                            CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Babham D., Brooks K., Chillingworth T., Commerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
Moniterica serovar Typhi CT18.";
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EMBL; AL627278; CAD07771.1; --
EMBL; AL627278; CAD07771.1; --
EMBL; AL627278; CAD07771.1; --
EMBL; AL627278; CAD07077.1; --
EMBL; AL627278; CAD07077.1; --
EMBL; AL62728; CAD070707.1; --
EMBL; AL62728; CAD070707.1; --
GO; GO:000842; F:2-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0016491; F:2-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0006416; F:phosphogluconate dehydrogenase (decarboxyla. . .;
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006513; P:valine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
                                                                                                                                                                                                                                                             248 ALEEAERLQLPVPGLSLAKBLYEELIKDGEENSGTQVLYKKYI 290
                                                                                                                                                                                                                                            510 AIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAYI 552
                                                                                                                                                                                                                                                                                                                                                                          01-MRR-2002 (TrEMBLrel. 20, Created)
01-MRR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60).
GARR OR STY3430 OR T3168.
                                                                                                                                                                                                                                                                                                                                                   294 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi
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                                                                                                                                                                                                                     329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Hander D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinsshi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                              Length 294;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                         F2DC91EF41EDEFAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 NALDISHGVGAQLPLTAAVMEMMQALRADGHGNDDHSAL 280
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Last annotation update)
                                                                         12.6%; Score 361; DB 16;
28.7%; Pred. No. 2.6e-17;
live 58; Mismatches 141;
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Oxidoreductase; Complete proteome
SEQUENCE 294 AA; 30468 MW; F2
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                                                                                                                                    80; Conservative
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                                                                                                          Local Similarity
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Query Match
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                                                                               .; IEA.
                                                                                                                                                                                                                                                        266 TDK-KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTC
                                                                                                                                                                                                                                                                                                DITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE
                                                                                                                                                                             12.5%; Score 357; DB 16; Length 296;
32.0%; Pred. No. 4.9e-17;
iive 47; Mismatches 137; Indels 16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=301 / Serotype 2a;
MEDLINE=22222406; PubMed=12384590;
MININE=22222406; PubMed=12384590;
Júin Q. Yuang Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang K., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Xan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R.. Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 DFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
                                        Nature 417:141-147(2002).

BMBL, AL939107; CAB62268.1; -.

GO, GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla., GO; GO:00066098; P:phosphogluconate shunt; IBA.

InterPro; IPR006115; 6PGD_NAD.

Pfan; PF03446; NAD_binding_2; 1.

Complete proteome. 296 AA; 30320 MW; DCBB9B266CE515A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=2457T / ATCC 700930 / Serotype 2a, MEDLINE=22590274; PubMed=12704152, MEDLINE=22590274; PubMed=12704152, Meb J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                 296 AA; 30320 MW; DCBB9B266CE515A5 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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YHAE OR SF3162 OR S3377
                                                                                                                                                                                             Local Similarity
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                               coelicolor A3(2).
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SEASINA-RBSO / ATCC BAA-588;

MINITINGA-22827954; PubMed=12910271;

RACHILL J. Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Chriman M., Arkin R., Baker S., Bason N., Cherevach I.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Numin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

RT Bordetella parapertussis and Bordetella bronchiseptica.";

RMED: BNBL; BX640449; CAE34588:1; -.
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                                                                        GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; GO:0004416; P:phosphogluconate dehydrogenase (decarboxyla. GO; GO:00046098; P:pentose-phosphate shunt; IEA. GO: GO:0006573; P:valine metabolism; IEA. InterPro; IPR002204; 3hydroxisobut_dh. InterPro; IPR006183; 6FGD. ND. InterPro; IPR006183; 6FGD. ND. InterPro; IPR006183; 6FGD. ND. InterPro; IPR006398; Tartro sem_red. Ffam; PF03446; ND. Indinging_2; I.
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Last annotation update)
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EMBL; AE015328;
EMBL; AE016989;
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                                                                                                                                                                                                                                                                         264 TPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE-GARLGRTPAEVVS
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Takami H., Takaki Y., Uchiyama L.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                            Gaps
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Nucleic Acids Res. 30:3927-3935(2002).
BMBL; AP004595; BAC12537.1;
GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .;
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
InterPro; IPR006115; 6PGD.
InterPro; IPR006115; 6PGD.
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Oceanobacillus.
NCBI_TaxID=182710;
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                                                                                                           DB 16; Length
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                                                                                                      12.4%; Score 354.5; DB 16; Length 29.6%; Pred. No. 7.6e-17; ive 58; Mismatches 134; Indels
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                     91AC4FBF73F6925F CRC64;
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; Pred. No. 9.5e-17;
56; Mismatches 148;
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                                  31326 MW;
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Best Local Similarity
                                      301 AA;
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                                  SEQUENCE
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                                      129 GDIGAESGTLAIMTGGERSVYDYVLPIFQVLGENISYQGPAĞTGQHTKASNQIALASNMI 188
                                                                                                                                                            189 GVCESLLYAKKAGLDPKKVLATISTGAAASFSLSKLGARMLENDFNPGFYVKHFIKDMRI 248
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390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22550857; PubMed=12663927;
Paulsen I.T., Banerjei L., Myers G.S., Nelson K.E., Seshadri R., Read T.D., Pouts D.E., Eisen D.A., Gill S.R., Heidelberg J.F., Tettelin H., Doddson R.J., Umayam L., Brinkac L., Beanan M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson Wanathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. GO; GO:0006098; P:pentose-phosphate shunt; IEA. InterPro; IPR006118; 6PGD. InterPro; IPR006118; 6PGD. Pfam; PF03446; NAD binding 2; Pfam; PF03446; NAD binding 2; Pfam; PR00076; 6PGDHDRGNĀSE.
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                     510 AIALGDAVNHPTPMAAAANEVYKRAKALDOSDNDMSAVYRA
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larity 29.9%; Pred. No. 1.5e-16;
Conservative 49; Mismatches 136;
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EMBL; AE016956; AAO82578.1; -.
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Search completed: September 16, 2004, 07:32:08 Job time : 54 secs

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190 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 227

AAO16415 standard; protein; 553

RESULT 2 AA016415 (first entry)

10-APR-2003

AA016415;

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The invention relates to human enzyme (ENZM) polypeptides and their corresponding polynucleotides. ENZM sequences are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional ENZM. The disorders include immune disorders (anaemia, allergy or asthma), infectious disorders (viral, fungal, parasitic or protozoal infection), immune deficiencies (acquired immune deficiency syndrome; ALDS), metabolic disorder (Addison's disease, diabetes or goiter), reproductive (disorders (Infertility or impotence), cardiovascular disorders (atherosclerosis or myocardial infarction), eye disorders and cell proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human enzyme (ENZM) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or
Aay99862 Escherich
Add95220 Alcaligen
                                                                                                                                                                                                                                                                                       Human; enzyme; ENZM; immune disorder; infection; myocardial infarction; gene therapy; anaemia; acquired immune deficiency syndrome; infection; reproductive disorder; cardiovascular; eye; cell proliferation; cancer; ALDS; allergy; asthma; Addison's disease; diabetes; goitre; imporence; infertility; atherosclerosis; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee SY, Ring HZ, Lee EA, Forsythe IJ, Khare R; hble AB, Richardson TW, Emerling BM, Lindquist EA; Hafalia AJA, Jin P, Swarnakar A, Li JX, Marquis JP; ad AB, Sprague WW, Becha SD, Elliott VS;
                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is human ENZM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 298-299; 264pp; English.
     AAY99862
ADD95220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overexpression of ENZM e.g. cancer.
                                                                                                                                                              AAE38240 standard; protein; 472 AA
                                                                                                                                                                                                                                                                Human enzyme (ENZM) protein #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-2001; 2001US-0340357P.
20-DEC-2001; 2001US-0342962P.
21-DEC-2001; 2001US-0343558P.
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Tran UK, Kaui.
Baughn MR, Hafalia A
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N-PSDB; AAD57520.
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Tran UK, Kable AE,
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       73
                                                                                                                                                                                                AAE38240;
                                                                                                                                            AAE38240
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The invention comprises the amino acid and coding sequences of human nucleic acid-associated proteins (NAAR). The DNA and protein sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of NAAP, such as: cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation); neurological disorders (e.g. Albibeimer's disease, Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders (e.g. Albs), allergies, asthma or Crohn's disease). The DNA sequences of the invention are useful for creating transgenic animals to model human disease. The present amino acid sequence represents a human nucleic acid-
                                                                                                                        Human; nucleic acid-associated protein; NAAP; arteriosclerosis; albS; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS; cancer; developmental disorder; renal tubular acidosis; anaemia; asthma; mental retardation; neurological disorder; Alzheimer's disease; epilepsy; parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; crohn's disease; transgenic animal; animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ree SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing, treating or preventing cell proliferative (e.g. cancer), neurological (e.g. epilepsy or Parkinson's disease), or autoimmune disorders (e.g. AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM; Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IJ; Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MR; Borowsky ML, Yao MG, Walia NK, Bandman O, Lal PG, Becha SD, Richardson TW, Elliott VS, Luo W, Tang YT, Zebarjadian Y, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid-associated proteins and polynucleotides, useful
                                                                                     Human nucleic acid-associated protein (NAAP) - SEQ ID No 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 1; Page 227-228; 312pp; English
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29-UN-2001; 2001US-03017879.
29-UN-2001; 2001US-0301892P.
29-UN-2001; 2001US-0301893P.
66-UU-2001; 2001US-0303405P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2002; 2002US-0364438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC.
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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38

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Gaps

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Indels

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Mismatches

0

Conservative

Local Similarity nes 38; Conserv

Matches

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Gaps

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Length 472; Indels

100.0%; Score 200; DB 6; 100.0%; Pred. No. 4.3e-20; 0; Mismatches

Best Local Similarity 100. Matches 38; Conservative

Query Match

AAW69240;

AAW69240 ID AAW6

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Human cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAB90667 - AAB90750. The cDNA clones are isolated from various classue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The collypeptides and nucleic acids may be used as nutrients or to modulate cyclokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences, proteins, their agonists and/or antagonists exhibit haematopoiesis regulating activity; tissue growth activity; activin/inhibin activity; cfemokinetic activity; haematopoiesis chemoteactic/chemokinetic activity; haematopoiesis activity; cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAP98490
                                                                              Human; secreted protein; nutrient; cytokine modulator; proliferation;
differentiation; immune system modulator; tissue growth; chemotactic;
haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids encoding polypeptides, useful for modulating ecytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins-Racie LA, Evans (Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human neoplastic disease associated polypeptide #123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.0%; Pred. No. 4.3e-15; 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 GFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                          Human AQ73_3 protein sequence SEQ ID 137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 468-470; 557pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.0%; Score 166;
                                                                                                                                                                                                                                                                                                                                                                                                                               Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bowman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU21690 standard; protein; 550 AA.
                                                                                                                                                                                                                                                                                                          14-SEP-2000; 2000WO-US025135.
                                                                                                                                                                                                                                                                                                                                                   99US-00398829.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccoy JM,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-244801/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 547 AA;
                                                                                                                                              haematopoiesis.
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                                                                                                                                                                                     Homo sapiens.
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Merberg D,
  07-JUN-2001
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                                                                                                                                                                                                                                                                                                                 Secreted protein; nutritional source; cell proliferation activity; cell differentiation activity; immune stimulant; tissue growth activator; haemacopoiesis regulator; anti-inflammatory; tumour invasion suppressor; tumour inhibitor; clone AQ73_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is secreted protein, encoded by a polymucleotide of the invention. The DNA was isolated from a human adult ovary CDNA library, and is designated clone AQ73 3. The DNA sequences and encoded polypeptides can be used as mutritional sources or supplements, or may immune stimulating or suppressing activity, haematopoiesis regulating activity, receptor/ligand activity, anti-inflammatory activity, activity, continuating or suppressor activity, inclinian activity, cadherin/inhibin activity, chemostatic/chemokinetic activity, cadherin/tumour invasion suppressor activity, tissue growth activity, tumour inhibition activity or other activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart cDNA libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treacy M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                             271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 308
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100.0%; Pred. No. 4.3e-15;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 66-67; 108pp; English.
                                                                                                                                                   AAW69240 standard; protein; 547 AA.
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97US-00989232.
                                                                                                                                                                                                                                  21-OCT-1998 (first entry)
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Spaulding V, Agostino MJ;
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les 32; Conservative
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Evans C;

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Gaps

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Length 547;

Human, neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder;

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AAB90720

AAB90720

Query Match

Best Loc Matches

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08-DEC-2000;
08-DEC-2000;
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11-DEC-2000;
       pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
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21-SEP-2000;
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07-JUN-2000;
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01-SEP-2000; 2000US-0229345P.
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2000US-0232399P.
2000US-0232400P.
2000US-0232401P.
2000US-0233063P.
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2000US-0220964P.
        22-MAR-2002; 2002US-00103313
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2000US-0225758P.
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2000US-0229345P.
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29-SEP-2000; 2000US-0236369P
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01-SEP-2000;
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18-AUG-2000;
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       The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA cases associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA cases associated polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders, reproductive disorders, gastrochinestinal disorders, pulmonary disorders, reproductive disorders, gastrochinestinal disorders. The polymucleotide sequences of the invention are also useful in gene therapy. AAUSIS68-AAUSI851 represent the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was for in interior.
                                                                                                                           Novel polypeptides and polynuclectides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neoplastic disease-associated polypeptide; gene therapy; hyperproliferative disease; cancer; autoimmune disorder; diabetes; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; sathma; eczema; inflammatory disorder; ischaemia-reperfusion injury; inflammatory bowel disease; Crohn's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; renal disorder; acute glomerulonephritis; end-stage renal disease; cardiovascular disorder; atherosclerosis; myocarditis; infectious disease; AlDS; cachexia; morexia; wound healing; epithelial cell proliferation; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.0%; Score 166; DB 4; Length 550; 100.0%; Pred. No. 4.3e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                    Claim 11; SEQ ID NO 417; 687pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC46331 standard; protein; 550 AA
                                                           Ruben SM
05-JAN-2001; 2001US-0259678P.
                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%;
les 32; Conservative 0
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                                                        Rosen CA, Barash SC,
                                                                                 WPI; 2001-465558/50.
                                                                                                  N-PSDB; AAS34889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 550 AA;
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Matches
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Barash SC;
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2000US-0246613P.
2000US-0249207P.
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2000US-0249209P.
2000US-0249210P.
2000US-0249211P.
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2000US-0249213P.
2000US-0249214P.
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2000US-0241221P.
2000US-0241785P.
2000US-0241786P.
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2000US-0237040P.
2000US-0239935P.
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2000US-0246478P.
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2000US-0249216P
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2000US-0249218P.
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N-PSDB; ADC46047.
                                                  13-OCT-2000; 2
20-OCT-2000; 2
20-OCT-2000; 2
20-OCT-2000; 2
20-OCT-2000; 2
20-OCT-2000; 2
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02-OCT-2000; 2
13-OCT-2000; 2
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05-DEC-2000;
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17-NOV-2000;
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The invention relates to one of 238 disclosed human neoplastic disease—
associated polypeptides encoded by 171 disclosed cDNA sequences
(including their domains, epitopes, full-length proteins,allelic variants
or species homologues). Also included are there encoding nucleic acids, a
crecombinant vector comprising the nucleic acid, a recombinant host cell
comprising the nucleic acid (expressing the protein), an isolated
comprising the nucleic acid (expressing the protein), an isolated
condition or ameliorating a medical condition, diagnosing a pathological
creating or ameliorating a medical condition, diagnosing a pathological
condition or a susceptibility to a pathological condition in a subject,
condition or a susceptibility to a pathological condition in a subject,
condition or a bolding partner to the polypeptide, identifying an activity
in a biological assay, and the gene corresponding to the cDNA sequence.
Creating, preventing, diagnosing, prognosticating, treating or
detecting, preventing, diagnosing, prognosticating, treating or
ameliorating medical conditions such as hyperproliferative diseases or
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
contained anneania) haematopoietic or haematologic disorders (e.g.
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        New isolated human neoplastic disease-associated polypeptides and polymucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anaemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.0%; Score 166; DB 7; L
100.0%; Pred. No. 4.3e-15;
iive 0; Mismatches 0;
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                                                                                                                   Claim 11; SEQ ID NO 417; 302pp; English.
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11-JUL-2000; 2000US-00614150.
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Matches 32; Conservative
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N-PSDB; ABL05033.
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                                                                                 disease
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ABB60930
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Disclosure; SEQ ID NO 9582; 21pp + Sequence Listing; English.

Length 161;

62.5%; Score 125; DB 7;

Sequence 161 AA;

Query Match

Matches

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGI76-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                   63.0%; Score 126; DB 4; Length 574; 60.5%; Pred. No. 2.8e-09; .ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                           Sequence 574 AA;
XXCCCCCCCCCCCXX
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Gaps
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                                   291 GFLGLGMMGSTIVKDLIYTGHKVVVWNRTIDKCQPFAE 328
                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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ABM74242 standard; protein; 161 AA

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(first entry)
  17-0CT-2003
 ABM74242;
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Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
DNA clone originating in barley containing SNP sequence #652.
                                                                                                                                                                                                                                                                         16-DEC-2002; 2002WO-IB005403.
                                                                                                                                                                 WO2003057877-A1.
                                                                                                            Hordeum vulgare.
                                                                                                                                                                                                                      17-JUL-2003
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20-DEC-2001; 2001JP-00387131. 20-DEC-2001; 2001JP-00403299. 20-DEC-2001; 2001JP-00403300. 27-SEP-2002; 2002JP-00327515 (UYNI-) UNIV JAPAN OKAYAMA.

2001JP-00387059

20-DEC-2001;

Kohara Y; Sato K, Takeda K,

WPI; 2003-587127/55.

Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired characteristics

Disclosure; SEQ ID XX; 284pp; Japanese.

barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonuclectides may be used for analysis of SNRs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published-pct-sequences The present invention relates to oligonuclectide clones originating in

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                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                Gaps
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8.16-10;
                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 51261.
                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                      64.7%; Prea. ...
                                                                                    AAG41222 standard; protein; 168 AA.
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990S-0130077P.
990S-0130449P.
990S-0130510P.
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99US-0132048P.
99US-0132407P.
99US-0132484P.
99US-0132485P.
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99US-0127462P.
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99US-0134370P.
99US-0134768P.
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99US-0137502P.
99US-0137724P.
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   Local Similarity 64.7 tes 22; Conservative
                                                                                                                                                                                      Arabidopsis thaliana.
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25-MAR-1999;
29-MAR-1999;
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06-APR-1999;
08-APR-1999;
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04-JUN-1999;
07-JUN-1999;
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05-MAY-1999;
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11-MAY-1999;
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21-APR-1999
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14-MAY-1999;
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                                                                                                    AAG41222;
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S-0138094P S-0138140P S-0138119P S-0139119P S-0139452P S-0139453P SS-0139453P SS-0139454 SS-0139456F SS-0139456F SS-0139458F SS-0139458F SS-0139458F SS-0139458F SS-0139458F SS-0139458F SS-0139458F SS-0139458F SS-0139458F	990S-0139750P. 990S-0139750P. 990S-0139877P. 990S-0139817P. 990S-014053P. 990S-0140659P. 990S-0140659P. 990S-0140659P. 990S-0140659P. 990S-0141287P. 990S-0141287P. 990S-0142154P. 990S-0142154P. 990S-0142154P. 990S-0142154P. 990S-0142154P. 990S-014239P. 990S-014239P. 990S-014333P. 990S-0144332P. 990S-0144333P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-0144334P. 990S-014508FP. 990S-014508FP. 990S-014508FP. 990S-0145145P. 990S-0145145P. 990S-0145145P. 990S-0145145P. 990S-0145134P.	30S-014638 30S-014638 30S-014703 30S-014730 90S-014719 90S-014719
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09-AUG-1999 09-AUG-1999 11-AUG-1999 12-AUG-1999 13-AUG-1999 13-AUG-1999 16-AUG-1999 17-AUG-1999 18-AUG-1999 20-AUG-1999	22 22 22 22 22 22 22 22 22 22 22 22 22	

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0; Gaps

Query Match 62.5%; Score 125; DB 3; Length 168; Best Local Similarity 60.5%; Pred. No. 8.5e-10; Matches 23; Conservative 4; Mismatches 11; Indels

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enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase; gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant; mouse-ear cress.
                                        Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide;

    A. thaliana gamma-hydroxybutyrate dehydrogenase homologue.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins related to gamma aminobutyric acid (GABA) metabolism, GABA-transaminase and gamma hydroxy butyrate dehydrogenase useful for screening and isolation of homologous genes from other organisms.
                                                                                                                                                                                                                                         Location/Qualifiers
1. .100
/note= "these residues are encoded by nucleotides 1-300"
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                                                                                                                                               Amino acid sequence of gamma-hydroxy butyrate dehydrogenase (GHBDH)
                                                                                                                                                                      Gamma-aminobutyric acid; GABA; GABA transaminase; GABA-T;
gamma-hydroxy butyrate dehydrogenase; GHBDH; succinic semialdehyde;
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 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
             4 GFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVE
                                                                                                                                                                                                                                                                                                                                                                                                         Van Cauwenberghe OR;
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Pred. No. 1.7e-09;
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                                                                             AAB19491 standard; protein; 289
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                                                                                                                                                                                              gamma hydroxybutyrate.
                                                                                                                                                                                                                    Arabidopsis thaliana
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N-PSDB; AAC62027.
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Matches
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Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrocopiase and UDP-glucosyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylenesuccinate semialdehyde, alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylene-gamma-aminobutyrate or alpha-methylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is mouse-ear cress (Arabidopsis thaliana) gamma-hydroxybutyrate dehydrogenase homologue
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3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
isovaleryl-CoA dehydrogenase; transgenic plant; soybean; EC 1.1.131.
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Pred. No. 1.7e-09;
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                                                                                                                                                                                                                                                                                                                                        Wang
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                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO (PRAB/) PRABHU V.
                                                                                                                                                                                                                                                                                                                                        Prabhu V,
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                                                                                                                                                    10-JUN-2002; 2002WO-US018230.
                                                                                                                                                                                                       08-JUN-2001; 2001US-0297198P.
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Arabidopsis thaliana,
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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38 

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AAE36392 standard; protein; 289 AA

RESULT 11

AAE36392

(first entry)

26-JUN-2003

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990S-0142154P-
99US-0142055P-
99US-014280P-
99US-0142803P-
99US-0142907P-
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99US-0140354P.
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9905-0135134P

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9905-0137522P

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28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
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                                                                                                                                                                                                  The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3 hydroxymethylgultaryl CoA (HMG-CoA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polymucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polymucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is soybean 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from ses2w.pk0002.e5 clone
                                                                                                                                                   Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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62.0%; Score 124; DB 5; Length 345;
Best Local Similarity 64.9%; Pred. No. 2.9e-09;
Matches 24; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 8740.
                                                                                                                                                                                                                                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                        55 GPLGLGIMGSPMAHNLLKAGVDLTVWNRTKSKCDPLI 91
                                                                                                  Rafalski JA;
                                                                               (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG10424 standard; protein; 343 AA
                                                                                                                                                                                    Claim 1; Col 33-36; 40pp; English
                                                                                                    Kinney AJ,
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99US-0123180P.
99US-012548P.
99US-0126264P.
99US-0126785P.
99US-0126785P.
99US-0128234P.
99US-0128234P.
99US-0128714P.
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                                                           98US-0094990P.
                                      99US-00364230
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                                                                                                    Cahoon RE, Hitz WD,
                                                                                                                      WPI; 2002-204621/26.
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                                                                                                                                    N-PSDB; AAD31750
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09-MAR-1999;
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29-MAR-1999;
01-APR-1999;
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14-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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                     990S-0159637P

990S-0159638P

990S-0160741P

990S-0160768P

990S-0160770P

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990S-0160814P

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990S-0160981P

990S-016098P

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The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylgiutaryl CoA (HWG-CoA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polynucleotides of the invention can be used as probes for physical mapping of ganomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from crln.pk0191.bl0, p0076.cwhan08r and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.
           or monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue
                                                                                                                                                                                                                                                                                                                                                                Branched chain amino acid degradation enzyme; HMG-CoA lyase;
3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.131.
                                                                                                                Length 290;
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                                                                                                                                         11; Indels
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                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                              Score 118; DB 6;
Pred. No. 1.7e-08;
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Pred. No. 3.1e-08;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rafalski JA;
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55.3%; Pred. No. ...
6; Mismatches
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                                                                                                                                                                                                                                                         AAE19927 standard; protein; 360 AA
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Best Local Similarity 63.69
....hes 21; Conservative
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                                                                                Sequence 290 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                US6348339-B1
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                                                                                                         Query Match
Best Local S
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                                                                                                                                 Matches
                                                                                                                                                                                                                              RESULT 16
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                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrogenase and UDP-glucosyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylenesuccinate semialdehyde, alphamethylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide;
enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase;
gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant.
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                    Score 123; DB 3; Length 353;
Pred. No. 4.1e-09;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue.
                                                                                                                                                                                                                                        4.1e-09;
                                                                                                                                                                                                                                                                                   1 GFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                    GFLGMGIMGSPMAQNLIKAGCDVTVWNRTKSKCD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 110-111; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                              AAE36391 standard; protein; 290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO
                         990S-016090P-
990S-016090P-
990S-016090P-
990S-0161404P-
990S-0161405P-
990S-0161405P-
990S-0161405P-
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                                                                                                                                     99US-0161360P.
                                                                                                                                                 99US-0161361P.
                                                                                                                                                                           99US-0161992P
                                                                                                                                                                                                                                  61.5%;
64.7%;
                                                                                                                                                                                                       99US-0162142P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-2002; 2002WO-US018230
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Damude HG, Flint D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-201331/19.
N-PSDB; AAD55024.
                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2002101013-A2
                                                                                                         25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intermediates.
                                                                                                                                                             28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                            21-OCT-1999
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                                       22-OCT-1999
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                                                                                                                                                                                                                                 Query Match
                                                                   22-OCT-1
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                                                      22-OCT
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Gaps

0;

Sequence 292 AA;

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression the 6213 antisense sequences given in the specification where expression of the 6213 antisense send inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that the san activity adainst a biological pathway the gene product or that has an activity against a biological pathway or equived for proliferation, or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits cellular proliferation of an ora gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound; a continuing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the strains or product is overexpressed or underexpressed; (12) determining the extent of the strains or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids activity, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, continuity in the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained to patent didentify from part of the printed specification, or patent did not form part of the prolifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #9686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 52083; 1766pp; English.
                                                        ABU24159 standard; protein; 292 AA
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                               Clostridium acetobutylicum
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Trawick JD,
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N-PSDB; ACA28029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277183-A2.
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08-FEB-2002;
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Wall |
RESULT 17
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: of the nucleic acid inhibits proliferation of a cell. Also included are: coding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding contisense nucleic acid; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which the test compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the biological contains a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the est compound that inhibits proliferation of an organism acts; (12) determining the extent product is overexpressed or underexpressed; (12) determining the extent product each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
                                  Gaps
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Length 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                  Indels
                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #2858.
                                    9
Score 109; DB 6;
Pred. No. 3.4e-07;
                                                                       1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTABK 32
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                                      6; Mismatches
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                                                                                                                                                                                                        ABU17331 standard; protein; 288
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0072851.
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54.5%;
                                                                                                                                                                                                                                                                                   19-JUN-2003 (first entry)
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                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Acinetobacter baumannii.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-029926/02.
                     Local Similarity
nes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277183-A2.
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Wall D,
     Query Match
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GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD

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identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumanni and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                          0
                                                                                                                                                                                                     53.0%; Score 106; DB 6; Length 288; 55.6%; Pred. No. 9.2e-07;
                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                    2 FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                       Pred. No. 9.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; SEQ ID NO 7407; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acinetobacter baumannii protein #3281.
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                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                  ADA36120 standard; protein; 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acinetobacter baumannii plant biocontrol agent.
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                                                                                                                                                                                                                Local Similarity
les 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Breton G, Bush D;
                                                                                                                                                                    Sequence 288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADA31994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6562958-B1.
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                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  ADA36120;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid of the nucleic acid antisense product operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway to proliferation, or that inhibits cellular proliferation of the pathway in which a proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or underexpressed; (12) determining the extent or compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the strains; or (13) identifying the target of a compound that inhibits for confleration of an organism. The antisense nucleic acids required for strains; or for screening for homologous nucleic acids required for glullar proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #2593
Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 44990; 1766pp; English.
                                                                                                              Ş
                                                                                                      ABU17066 standard; protein; 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                 Acinetobacter baumannii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACA20936
                                                                                                                                                                                                                                                                                                                                        WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001;
                                                                                                                                                                                    19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002
                                                                                                                                            ABU17066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang L,
Wall D,
                                                                     RESULT
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Gaps

0;

10; Indels

53.0%; Score 106; DB 6; Length 299; 25.9%; Pred. No. 9.6e-07; Conservative 6; Mismatches 10; Indels

Query Match Best Local Similarity Matches 18; Conserv

baumannii protein.

Sequence 299 AA;

6; Mismatches

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18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-1999
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                                                                                                                                                                                         06-SEP-2000.
                                                                                                                                                                                                                                                                                                                       16-APR-1999;
                                                                                                                                                                                                                                                                                                                                          21-APR-1999;
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                                                                                                                                                                                                                              25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                         05-MAR-1999
09-MAR-1999
                                                                                                                                                                                                                                                                               29-MAR-1999
                                                                                                                                                                                                                                                                                          01-APR-1999
                                                                   17-OCT-2000
                                                AAG10425;
          RESULT 22
                    AAG10425
                                                ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial Avacines, as targets for antibacterial furgs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                           Gaps
                                                                                                                                                                                                                                                              baumannii; bacterial disease; antibacterial; vaccine;
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                                                                       Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                           Indels
                                                              Score 105; DB 6; Le
Pred, No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 FLGIGLMGSRMASRLIQAGFQVAVWNRTTSACEELI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                GPVGTGIMGMPMAMNLLKAGHOVKVWNRTSSK 36
                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
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                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; SEQ ID NO 8139; 328pp; English.
                                                                                                                                                                                                                                             Acinetobacter baumannii protein #4013.
                                                                                                                                                                                    ADA36852 standard; protein; 326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.0%;
                                                                        52.5%;
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                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 52.8
Matches 19; Conservative
                                                                                             Conservative
                                                                                                                                                                                                                                                                                               Acinetobacter baumannii.
                                                                                                                                                                                                                                                                             plant biocontrol agent
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                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bush D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 326 AA;
                                                      Sequence 290 AA;
                                                                                                                                                                                                                                                                   Acinetobacter
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                                                                                                                                                                                                         ADA36852;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 8741.
AAG10425 standard; protein; 285 AA.
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9905-0132485F.
9905-0132486F.
9905-0132487F.
9905-0132663F.
9905-0134256F.
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990S-0134221P.
990S-0134370P.
990S-0134768P.
990S-0134941P.
990S-0135353P.
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99US-0139456P.
99US-0139457P.
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99US-0137528P.
99US-0137502P.
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99US-0126264P.
99US-0126785P.
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99US-0123180P.
99US-0123548P.
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                                                                                                                                                                                                                                                                 25-FEB-2000; 2000EP-00301439
                                                          (first entry)
                                                                                                                                                    termination sequence
                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
                                                                                                                                                                                                             EP1033405-A2.
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PR 18—707—1999) 9902—0139458P.

PR 18—707—1999) 9902—0139458P.

PR 18—707—1999) 9902—0139452P.

PR 18—707—1999) 9902—0139452P.

PR 22—707—1999) 9902—0139452P.

PR 22—707—1999) 9902—0139452P.

PR 22—707—1999) 9902—0139452P.

PR 22—707—1999) 9902—0139452P.

PR 22—707—1999) 9902—0139432P.

PR 23—707—1999) 9902—0139432P.

PR 23—707—1999) 9902—0139432P.

PR 23—707—1999) 9902—014392P.

PR 23—707—1999) 9902—014392P.

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PR 23—707—1999) 9902—014392P.

PR 23—707—1999) 9902—014332P.

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PR 23—707—1999) 9902—014332P.

PR 23—707—1999) 9902—014332P.

PR 23—707—1999) 9902—014332P.

PR 23—707—1999) 9903—014332P.

PR 23—707—1999) 9903—014332P.

PR 23—707—1999) 9903—014332P.

PR 23—707—1999) 9903—014332P.

PR 23—707—1999) 9903—014332P.

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PR 23—707—1999) 9903—014332P.

PR 23—707—1999) 9903
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Gaps
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ABU29967
ID ABU29967 standard; protein; 295 AA.
XX
AC ABU29967;
990S-0149723P.
990S-0149902P.
990S-0149930P.
990S-015066P.
990S-0151066P.
990S-0151068P.
990S-015108P.
990S-015130P.
990S-015130P.
990S-015130P.
990S-015130P.
990S-0154018P.
990S-0154018P.
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990S-0154018P.
990S-0155139P.
990S-0155139P.
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990S-0156139P.
990S-015628P.
990S-015628P.
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990S-015628P.
990S-015628P.
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990S-0160741P

990S-016076P

990S-016070P

990S-016081AP

990S-0160981P

990S-0160981P

990S-0160981P

990S-0161981P

990S-0161981P

990S-0161981P

990S-016190P

990S-0161361P

990S-0161361P

990S-0161361P

990S-0161920P

990S-0161920P

990S-0161920P
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
                                                                                                                                                                          04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
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14-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

22-007-1999

22-007-1999

25-007-1999

25-007-1999

26-007-1999

26-007-1999

28-007-1999

28-007-1999

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28-007-1999
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Matches
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N-PSDB; ACA33837
          WO200277183-A2.
                                                                                 electronic
                  21-MAR-2001;
19-JUN-2003
            03-OCT-2002
                            Wang L,
Wall D,
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New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                       Vaccine, urinary tract infection; bacteraemia; endocarditis; wound;
4 GFIGTGVMGSAVARHLLEAGHEVAVYNRTKAKAD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 5109; 243pp; English.
                                                                                                                                                                                                                                                                                E. faecium protein sequence SEQ ID 5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                           ADC95482 standard; protein; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0051571P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bush D;
                                                                                                                                                                                                                                                                                                                                                      abdominal-pelvic infection
                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADC91828.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                            ADC95482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                     RESULT 24
                                                                                                                          ADC95482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention trained to an instance, in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(i) a weetor comprising a promoter operably linked to the nucleic acid inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated are:

(i) a vector comprising a promoter operably linked to the nucleic acid; (4) an antibody apable of specifically binding attributed by the molypeptide or its fragment whose expression is inhibited by the attributed of a proliferation or the activity of agene in an operon required for proliferation or the activity of agene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which the test compound that inhibits proliferation of an or that inhibits proliferation of an or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of strains; or (13) identifying the expensent in a culture or collection of an organism. The anisense nucleic acids are useful for the strains or activity of hownloaders are as the propertion of an organism. The anisense nucleic acids are useful for the strains or active are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational derug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid comprising any one of
                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                         Protein encoded by Prokaryotic essential gene #15494.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 57891; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                             06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-034293P.
08-FSB-2002; 2002US-0362891.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone
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                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zamudio C,
Trawick JD,
                                                                                                                                                       Enterococcus faecium.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 295 AA;
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Enterococcus facetium encoding an Enterococcus facetium polypeptide

Enterococcus facetium encoding an Enterococcus facetium polypeptide

Co one of 10 fully defined sequences given in the (or comprising 40

Co complement or sequences hybridising to it). Also included are a

Co complement or sequences hybridising to it). Also included are a

crecombinant vector comprising the nucleic acid operably linked to

transcription regulatory element, a cell comprising the vector and a

crecombinant vector comprising the nucleic acid. The nucleic acids are

crecombined probe comprising the nucleic acid. The nucleic acids are

cresulting from E. facetium bacterial infection (e.g. urinary tract

resulting from E. facetium to recept in the crion of conditions

cresulting from E. facetium bacterial infection of e.g. urinary tract

infection, bacteraemia, endocarditis, wounds and abdominal-pelvic

infection, and for screening drugs such as agonists and antagonists. The

concleic acid is useful for recombinant production of Candida albicans

derived peptides or antisense polypeptides. Pharmaccutical compositions

and vaccines containing the nucleic acid are useful for preventing or

treating Enterococcus facetium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 299;
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larity 52.9%; Pred. No. 7.1e-06;
Conservative 6; Mismatches 10;
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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34

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99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
99US-0128714P.
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99US-0130510P.
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99US-014287P.
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99US-0143624P.
99US-0144005P.
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
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23-APR-1999;
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30-APR-1999;
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24 - MAY - 1999;
25 - MAY - 1999;
27 - MAY - 1999;
01 - JUN - 1999;
04 - JUN - 1999;
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18-JUN-1999;
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13-JUL-1999;
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14-MAY-1999
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18-MAY-1999
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08-JUN-1999
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      ·;
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                                                                                                                                                                                                                                          6-phospho:gluconate dehydrogenase - can be recombinantly produced by transforming coryneform bacteria with DNA molecule encoding it.
                                                                                                                                                                                                                                                                                      The present sequence is the Brevibacterium flavum JM-233 6-phosphogluconate dehydrogenase (6-PD). The 6-PD can be recombinantly produced by transforming coryneform bacteria with the DNA molecule encoding it
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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45.9%; Pred. No. 0.00013;
vative 7; Mismatches 13; Indels
                                                                              Brevibacterium flavum; 6-phosphogluconate dehydrogenase; recombinant production; coryneform; bacterium; bacteria.
                                                            Brevibacterium flavum 6-phosphogluconate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 3182.
                                                                                                                                                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                 AAW27613 standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG06417 standard; protein; 158 AA
                                                                                                                                                                                                                                                                    Claim 1; Page 5-7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0121825P.
99US-0123180P.
99US-0123548P.
                                                                                                                                                              96JP-00036346
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                                                                                                                                                                               96JP-00036346
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                                           22-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.99
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2000 (first entry)
                                                                                                         Brevibacterium flavum
                                                                                                                                                                                                                 WPI; 1997-484097/45.
N-PSDB; AAT88035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           termination sequence
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                                                                                                                                                                                                                                                                                                                                   Sequence 492 AA;
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                                                                                                                                                            23-FEB-1996;
                                                                                                                                                                              23-FEB-1996;
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05-MAR-1999;
09-MAR-1999;
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                           AAW27613;
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AAG06417
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99US-0144085P.
99US-0144331P.
99US-0144331P.
99US-0144331P.
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99US-014731B.
99US-014731B.
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9905-0149723P.
9905-0149902P.
9905-0149902P.
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9905-015403P.
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26-AUG-1999;
27-AUG-1999;
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37-AUG-1999;
31-AUG-1999;
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05-AUG-1999;
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09-AUG-1999;
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27-JUL-1999;
27-JUL-1999;
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13-SEP-1999;
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07-SEP-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 3181.
                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLXMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                          'Match 46.0%; Score 92; DB Cocal Similarity 45.9%; Pred. No. 4.7e-
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                                                                                                                                                                                                                                                                                                                                                                             AAG06416 standard; protein; 180
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99US-0123180P.
99US-012548P.
99US-0125784P.
99US-0125785P.
99US-0127462P.
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9905-0159299-
9905-0159294-
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9905-0159290-
9905-0159310-
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9905-0159310-
9905-0159584-
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990S-0161405P.
990S-0161359P.
990S-0161359P.
990S-0161360P.
990S-0161361P.
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99US-0161993P.
99US-0162142P.
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99US-0158029P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    termination sequence
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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16-APR-1999;
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22-0CT-1999;
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21-0CT-1999;
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Matches
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                                                                                                                                                                                             46.0%; Score 92; DB 3; Length 180;
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Pred. No. 5.5e-05;
8; Mismatches 12;
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llarity 45.9%;
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Query Match

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